

NUCLEIC ACIDS CONTAINING SINGLE NUCLEOTIDE POLYMORPHISMS AND METHODS OF USE THEREOF

RELATED APPLICATIONS

This application claims priority to U.S.S.N. 60/167,383, filed November 24, 1999, which is incorporated herein by reference in its entirety.

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BACKGROUND OF THE INVENTION

Sequence polymorphism-based analysis of nucleic acid sequences can augment or replace previously known methods for determining the identity and relatedness of individuals. The approach is generally based on alterations in nucleic acid sequences between related individuals. This analysis has been widely used in a variety of genetic, diagnostic, and forensic applications. For example, polymorphism analyses are used in identity and paternity analysis, and in genetic mapping studies.

One such type of variation is a restriction fragment length polymorphism (RFLP). RFLPS can create or delete a recognition sequence for a restriction endonuclease in one nucleic acid relative to a second nucleic acid. The result of the variation is an alteration in the relative length of restriction enzyme generated DNA fragments in the two nucleic acids.

Other polymorphisms take the form of short tandem repeats (STR) sequences, which are also referred to as variable numbers of tandem repeat (VNTR) sequences. STR sequences typically include tandem repeats of 2, 3, or 4 nucleotide sequences that are present in a nucleic acid from one individual but absent from a second, related individual at the corresponding genomic location.

Other polymorphisms take the form of single nucleotide variations, termed single nucleotide polymorphisms (SNPs), between individuals. A SNP can, in some instances, be referred to as a "cSNP" to denote that the nucleotide sequence containing the SNP

originates as a cDNA.

SNPs can arise in several ways. A single nucleotide polymorphism may arise due to a substitution of one nucleotide for another at the polymorphic site. Substitutions can be transitions or transversions. A transition is the replacement of one purine nucleotide
5 by another purine nucleotide, or one pyrimidine by another pyrimidine. A transversion is the replacement of a purine by a pyrimidine, or the converse.

Single nucleotide polymorphisms can also arise from a deletion of a nucleotide or an insertion of a nucleotide relative to a reference allele. Thus, the polymorphic site is a site at which one allele bears a gap with respect to a single nucleotide in another allele.
10 Some SNPs occur within, or near genes. One such class includes SNPs falling within regions of genes encoding for a polypeptide product. These SNPs may result in an alteration of the amino acid sequence of the polypeptide product and give rise to the expression of a defective or other variant protein. Such variant products can, in some cases result in a pathological condition, *e.g.*, genetic disease. Examples of genes in which
15 a polymorphism within a coding sequence gives rise to genetic disease include sickle cell anemia and cystic fibrosis. Other SNPs do not result in alteration of the polypeptide product. Of course, SNPs can also occur in noncoding regions of genes.

SNPs tend to occur with great frequency and are spaced uniformly throughout the genome. The frequency and uniformity of SNPs means that there is a greater probability
20 that such a polymorphism will be found in close proximity to a genetic locus of interest.

SUMMARY OF THE INVENTION

The invention is based in part on the discovery of novel single nucleotide polymorphisms (SNPs) in regions of human DNA.

Accordingly, in one aspect, the invention provides an isolated polynucleotide
25 which includes one or more of the SNPs described herein. The polynucleotide can be, *e.g.*, a nucleotide sequence which includes one or more of the polymorphic sequences shown in Table 1 and the Sequence Listing (SEQ ID NOS: 1 - 1468) and which includes a polymorphic sequence, or a fragment of the polymorphic sequence, as long as it

includes the polymorphic site. The polynucleotide may alternatively contain a nucleotide sequence which includes a sequence complementary to one or more of the sequences (SEQ ID NOS: 1-1468), or a fragment of the complementary nucleotide sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence.

5 The polynucleotide can be, *e.g.*, DNA or RNA, and can be between about 10 and about 100 nucleotides, *e.g.*, 10-90, 10-75, 10-51, 10-40, or 10-30, nucleotides in length.

 In some embodiments, the polymorphic site in the polymorphic sequence includes a nucleotide other than the nucleotide listed in Table 1, column 5 for the polymorphic sequence, *e.g.*, the polymorphic site includes the nucleotide listed in Table 1, column 6
10 for the polymorphic sequence.

 In other embodiments, the complement of the polymorphic site includes a nucleotide other than the complement of the nucleotide listed in Table 1, column 5 for the complement of the polymorphic sequence, *e.g.*, the complement of the nucleotide listed in Table 1, column 6 for the polymorphic sequence.

15 In some embodiments, the polymorphic sequence is associated with a polypeptide related to one of the protein families disclosed herein. For example, the nucleic acid may be associated with a polypeptide related to an ATPase associated protein, a cadherin, or any of the other proteins identified in Table 1, column 10.

 In another aspect, the invention provides an isolated allele-specific
20 oligonucleotide that hybridizes to a first polynucleotide containing a polymorphic site. The first polynucleotide can be, *e.g.*, a nucleotide sequence comprising one or more polymorphic sequences (SEQ ID NOS:1 - 1468), provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for the polymorphic sequence. Alternatively, the first polynucleotide can be a nucleotide
25 sequence that is a fragment of the polymorphic sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence, or a complementary nucleotide sequence which includes a sequence complementary to one or more polymorphic sequences (SEQ ID NOS:1 - 1468), provided that the complementary nucleotide

sequence includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5. The first polynucleotide may in addition include a nucleotide sequence that is a fragment of the complementary sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence.

5 In some embodiments, the oligonucleotide does not hybridize under stringent conditions to a second polynucleotide. The second polynucleotide can be, *e.g.*, (a) a nucleotide sequence comprising one or more polymorphic sequences (SEQ ID NOS:1 - 1468), wherein the polymorphic sequence includes the nucleotide listed in Table 1, column 5 for the polymorphic sequence; (b) a nucleotide sequence that is a fragment of
10 any of the polymorphic sequences; (c) a complementary nucleotide sequence including a sequence complementary to one or more polymorphic sequences (SEQ ID NOS:1 - 1468), wherein the polymorphic sequence includes the complement of the nucleotide listed in Table 1, column 5; and (d) a nucleotide sequence that is a fragment of the complementary sequence, provided that the fragment includes a polymorphic site in the
15 polymorphic sequence.

The oligonucleotide can be, *e.g.*, between about 10 and about 100 bases in length. In some embodiments, the oligonucleotide is between about 10 and 75 bases, 10 and 51 bases, 10 and about 40 bases, or about 15 and 30 bases in length.

The invention also provides a method of detecting a polymorphic site in a nucleic
20 acid. The method includes contacting the nucleic acid with an oligonucleotide that hybridizes to a polymorphic sequence selected from the group consisting of SEQ ID NOS: 1-1468, or its complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for the polymorphic sequence, or the complement includes a nucleotide other than the complement of the
25 nucleotide recited in Table 1, column 5. The method also includes determining whether the nucleic acid and the oligonucleotide hybridize. Hybridization of the oligonucleotide to the nucleic acid sequence indicates the presence of the polymorphic site in the nucleic acid.

In preferred embodiments, the oligonucleotide does not hybridize to the polymorphic sequence when the polymorphic sequence includes the nucleotide recited in Table 1, column 5 for the polymorphic sequence, or when the complement of the polymorphic sequence includes the complement of the nucleotide recited in Table 1, column 5 for the polymorphic sequence.

The oligonucleotide can be, *e.g.*, between about 10 and about 100 bases in length. In some embodiments, the oligonucleotide is between about 10 and 75 bases, 10 and 51 bases, 10 and about 40 bases, or about 15 and 30 bases in length.

In some embodiments, the polymorphic sequence identified by the oligonucleotide is associated with a polypeptide related to one of the protein families disclosed herein. For example, the nucleic acid may be associated polypeptide related to an ATPase associated protein, cadherin, or any of the other protein families identified in Table 1, column 10.

In another aspect, the method includes determining if a sequence polymorphism is the present in a subject, such as a human. The method includes providing a nucleic acid from the subject and contacting the nucleic acid with an oligonucleotide that hybridizes to a polymorphic sequence selected from the group consisting of SEQ ID NOS: 1-1468, or its complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5. Hybridization between the nucleic acid and the oligonucleotide is then determined. Hybridization of the oligonucleotide to the nucleic acid sequence indicates the presence of the polymorphism in said subject.

In a further aspect, the invention provides a method of determining the relatedness of a first and second nucleic acid. The method includes providing a first nucleic acid and a second nucleic acid and contacting the first nucleic acid and the second nucleic acid with an oligonucleotide that hybridizes to a polymorphic sequence selected from the group consisting of SEQ ID NOS: 1-1468, or its complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1,

column 5 for the polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5. The method also includes determining whether the first nucleic acid and the second nucleic acid hybridize to the oligonucleotide, and comparing hybridization of the first and second nucleic acids to the oligonucleotide. Hybridization of first and second nucleic acids to the nucleic acid indicates the first and second subjects are related.

In preferred embodiments, the oligonucleotide does not hybridize to the polymorphic sequence when the polymorphic sequence includes the nucleotide recited in Table 1, column 5 for the polymorphic sequence, or when the complement of the polymorphic sequence includes the complement of the nucleotide recited in Table 1, column 5 for the polymorphic sequence.

The oligonucleotide can be, *e.g.*, between about 10 and about 100 bases in length. In some embodiments, the oligonucleotide is between about 10 and 75 bases, 10 and 51 bases, 10 and about 40 bases, or about 15 and 30 bases in length.

The method can be used in a variety of applications. For example, the first nucleic acid may be isolated from physical evidence gathered at a crime scene, and the second nucleic acid may be obtained from a person suspected of having committed the crime. Matching the two nucleic acids using the method can establish whether the physical evidence originated from the person.

In another example, the first sample may be from a human male suspected of being the father of a child and the second sample may be from the child. Establishing a match using the described method can establish whether the male is the father of the child.

In another aspect, the invention provides an isolated polypeptide comprising a polymorphic site at one or more amino acid residues, and wherein the protein is encoded by a polynucleotide including one of the polymorphic sequences SEQ ID NOS:1-1468, or their complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for the polymorphic sequence, or the

complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5.

The polypeptide can be, *e.g.*, related to one of the protein families disclosed herein. For example, polypeptide can be related to an ATPase associated protein,
5 cadherin, or any of the other proteins provided in Table 1, column 10.

In some embodiments, the polypeptide is translated in the same open reading frame as is a wild type protein whose amino acid sequence is identical to the amino acid sequence of the polymorphic protein except at the site of the polymorphism.

In some embodiments, the polypeptide encoded by the polymorphic sequence, or
10 its complement, includes the nucleotide listed in Table 1, column 6 for the polymorphic sequence, or the complement includes the complement of the nucleotide listed in Table 1, column 6.

The invention also provides an antibody that binds specifically to a polypeptide encoded by a polynucleotide comprising a nucleotide sequence encoded by a
15 polynucleotide selected from the group consisting of polymorphic sequences SEQ ID NOS:1-1468, or its complement. The polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for the polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5.

20 In some embodiments, the antibody binds specifically to a polypeptide encoded by a polymorphic sequence which includes the nucleotide listed in Table 1, column 6 for the polymorphic sequence.

Preferably, the antibody does not bind specifically to a polypeptide encoded by a polymorphic sequence which includes the nucleotide listed in Table 1, column 5 for the
25 polymorphic sequence.

The invention further provides a method of detecting the presence of a polypeptide having one or more amino acid residue polymorphisms in a subject. The

method includes providing a protein sample from the subject and contacting the sample with the above-described antibody under conditions that allow for the formation of antibody-antigen complexes. The antibody-antigen complexes are then detected. The presence of the complexes indicates the presence of the polypeptide.

5 The invention also provides a method of treating a subject suffering from, at risk for, or suspected of, suffering from a pathology ascribed to the presence of a sequence polymorphism in a subject, *e.g.*, a human, non-human primate, cat, dog, rat, mouse, cow, pig, goat, or rabbit. The method includes providing a subject suffering from a pathology associated with aberrant expression of a first nucleic acid comprising a polymorphic
10 sequence selected from the group consisting of SEQ ID NOS:1 - 1468, or its complement, and treating the subject by administering to the subject an effective dose of a therapeutic agent. Aberrant expression can include qualitative alterations in expression of a gene, *e.g.*, expression of a gene encoding a polypeptide having an altered amino acid sequence with respect to its wild-type counterpart. Qualitatively different polypeptides
15 can include, shorter, longer, or altered polypeptides relative to the amino acid sequence of the wild-type polypeptide. Aberrant expression can also include quantitative alterations in expression of a gene. Examples of quantitative alterations in gene expression include lower or higher levels of expression of the gene relative to its wild-type counterpart, or alterations in the temporal or tissue-specific expression pattern of a gene. Finally,
20 aberrant expression may also include a combination of qualitative and quantitative alterations in gene expression.

 The therapeutic agent can include, *e.g.*, second nucleic acid comprising the polymorphic sequence, provided that the second nucleic acid comprises the nucleotide present in the wild type allele. In some embodiments, the second nucleic acid sequence
25 comprises a polymorphic sequence which includes nucleotide listed in Table 1, column 5 for the polymorphic sequence.

 Alternatively, the therapeutic agent can be a polypeptide encoded by a polynucleotide comprising polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 1468, or by a polynucleotide comprising a nucleotide sequence that is

complementary to any one of polymorphic sequences SEQ ID NOS:1 - 1468, provided that the polymorphic sequence includes the nucleotide listed in Table 1, column 6 for the polymorphic sequence.

The therapeutic agent may further include an antibody as herein described, or an oligonucleotide comprising a polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 1468, or by a polynucleotide comprising a nucleotide sequence that is complementary to any one of polymorphic sequences SEQ ID NOS:1 - 1468, provided that the polymorphic sequence includes the nucleotide listed in Table 1, column 5 or Table 1, column 6 for the polymorphic sequence.

In another aspect, the invention provides an oligonucleotide array comprising one or more oligonucleotides hybridizing to a first polynucleotide at a polymorphic site encompassed therein. The first polynucleotide can be, *e.g.*, a nucleotide sequence comprising one or more polymorphic sequences (SEQ ID NOS:1 - 1468); a nucleotide sequence that is a fragment of any of the nucleotide sequences, provided that the fragment includes a polymorphic site in the polymorphic sequence; a complementary nucleotide sequence comprising a sequence complementary to one or more polymorphic sequences (SEQ ID NOS:1 - 1468); or a nucleotide sequence that is a fragment of the complementary sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence.

In preferred embodiments, the array comprises 10; 100; 1,000; 10,000; 100,000 or more oligonucleotides.

The invention also provides a kit comprising one or more of the herein-described nucleic acids. The kit can include, *e.g.*, a polynucleotide which includes one or more of the SNPs described herein. The polynucleotide can be, *e.g.*, a nucleotide sequence which includes one or more of the polymorphic sequences shown in Table 1 and the Sequence Listing (SEQ ID NOS: 1 - 1468) and which includes a polymorphic sequence, or a fragment of the polymorphic sequence, as long as it includes the polymorphic site. The polynucleotide may alternatively contain a nucleotide sequence which includes a sequence complementary to one or more of the sequences (SEQ ID NOS:1-1468), or a

fragment of the complementary nucleotide sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence. The invention provides an isolated allele-specific oligonucleotide that hybridizes to a first polynucleotide containing a polymorphic site. The first polynucleotide can be, *e.g.*, a nucleotide sequence comprising one or more polymorphic sequences (SEQ ID NOS:1 - 1468), provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for the polymorphic sequence. Alternatively, the first polynucleotide can be a nucleotide sequence that is a fragment of the polymorphic sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence, or a complementary nucleotide sequence which includes a sequence complementary to one or more polymorphic sequences (SEQ ID NOS:1 - 1468), provided that the complementary nucleotide sequence includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5. The first polynucleotide may in addition include a nucleotide sequence that is a fragment of the complementary sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, suitable methods and materials are described below. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In the case of conflict, the present specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting.

Other features and advantages of the invention will be apparent from the following detailed description and claims.

DETAILED DESCRIPTION OF THE INVENTION

The invention provides human SNPs in sequences which are transcribed, *i.e.*, are cSNPs. As is explained in more detail below, many SNPs have been identified in genes related to polypeptides of known function. For some applications, SNPs associated with various polypeptides can be used together. For example, SNPs can be group according to whether they are derived from a nucleic acid encoding a polypeptide related to a particular protein family or involved in a particular function. Thus, SNPs related to ATPase associated protein may be collected for some applications, as may SNPs associated with cadherin, or ephrin (EPH), or any of the other proteins recited in Table 1, column 10. Similarly, SNPs can be grouped according to the functions played by their gene products. Such functions include, e.g., structural proteins, proteins from which associated with metabolic pathways fatty acid metabolism, glycolysis, intermediary metabolism, calcium metabolism, proteases, and amino acid metabolism.

The SNPs are shown in Table 1 and the Sequence Listing. Both provide a summary of the polymorphic sequences disclosed herein. In the Table, a "SNP" is a polymorphic site embedded in a polymorphic sequence. The polymorphic site is occupied by a single nucleotide, which is the position of nucleotide variation between the wild type and polymorphic allelic sequences. The site is usually preceded by and followed by relatively highly conserved sequences of the allele (e.g., sequences that vary in less than 1/100 or 1/1000 members of the populations). Thus, a polymorphic sequence can include one or more of the following sequences: (1) a sequence having the nucleotide denoted in Table 1, column 5 at the polymorphic site in the polymorphic sequence; or (2) a sequence having a nucleotide other than the nucleotide denoted in Table 1, column 5 at the polymorphic site in the polymorphic sequence. An example of the latter sequence is a polymorphic sequence having the nucleotide denoted in Table 1, column 6 at the polymorphic site in the polymorphic sequence.

Nucleotide sequences for a referenced-polymorphic pair are presented in Table 1. Each cSNP entry provides information concerning the wild type nucleotide sequence as well as the corresponding sequence that includes the SNP at the polymorphic site. Since

the wild type sequence is already known, the Sequence Listing accompanying this application provides only the sequence of the polymorphic allele; its SEQ ID NO: is also cross referenced in the Table 1. A reference to the SEQ ID NO: giving the translated amino acid sequence is also given if appropriate. The Table includes thirteen columns that provide descriptive information for each cSNP, each of which occupies one row in the Table. The column headings, and an explanation for each, are given below.

“SEQ ID” provides the cross-reference to the nucleotide SEQ ID NO:, and, as explained below, an amino acid SEQ ID NO: as well, in the Sequence Listing of the application. Conversely, each sequence entry in the Sequence Listing also includes a cross-reference to the CuraGen sequence ID, under the label “CuraGen Sequence ID”. The first SEQ ID NO: given in the first column of each row of the Table is the SEQ ID NO: identifying the nucleic acid sequence for the polymorphism. If a polymorphism carries an entry for the amino acid portion of the row, a second SEQ ID NO: appears in parentheses in the column “Amino acid after” (see below). This second SEQ ID NO: refers to an amino acid sequence giving the polymorphic amino acid sequence that is the translation of the nucleotide polymorphism. If a polymorphism carries no entry for the protein portion of the row, only one SEQ ID NO: is provided.

“CuraGen sequence ID” provides CuraGen Corporation’s accession number.

“Base pos. of SNP” gives the numerical position of the nucleotide in the reference, or wild-type, gene at which the cSNP is found. This enumeration of bases is that found in the public database from which the reference gene is taken (see column headed “Name of protein identified following a BLASTX analysis of the CuraGen sequence”) as of the filing date of the instant application.

“Polymorphic sequence” provides a 51-base sequence with the polymorphic site at the 26th base in the sequence, as well as 25 bases from the reference sequence on the 5’ side and the 3’ side of the polymorphic site. The designation at the polymorphic site is enclosed in square brackets, and provides first, the reference nucleotide; second, a “slash (/)”; and third, the polymorphic nucleotide. In certain cases the polymorphism is an

insertion or a deletion. In that case, the position which is “unfilled” (i.e., the reference or the polymorphic position) is indicated by the word “gap”.

“Base before” provides the nucleotide present in the reference, or wild-type, gene at the position at which the polymorphism is found.

5 “Base after” provides the altered nucleotide at the position of the polymorphism.

“Amino acid before” provides the amino acid in the reference protein, if the polymorphism occurs in a coding region.

10 “Amino acid after” provides the amino acid in the polymorphic protein, if the polymorphism occurs in a coding region. This column also includes the SEQ ID NO: in parentheses if the polymorphism occurs in a coding region.

“Type of change” provides information on the nature of the polymorphism.

“SILENT-NONCODING” is used if the polymorphism occurs in a noncoding region of a nucleic acid.

15 “SILENT-CODING” is used if the polymorphism occurs in a coding region of a nucleic acid of a nucleic acid and results in no change of amino acid in the translated polymorphic protein.

“CONSERVATIVE” is used if the polymorphism occurs in a coding region of a nucleic acid and provides a change in which the altered amino acid falls in the same class as the reference amino acid. The classes are:

20 Aliphatic: Gly, Ala, Val, Leu, Ile;

Aromatic: Phe, Tyr, Trp;

Sulfur-containing: Cys, Met;

Aliphatic OH: Ser, Thr;

Basic: Lys, Arg, His;

Acidic: Asp, Glu, Asn, Gln;

Pro falls in none of the other classes; and

End defines a termination codon.

5 “NONCONSERVATIVE” is used if the polymorphism occurs in a coding region of a nucleic acid and provides a change in which the altered amino acid falls in a different class than the reference amino acid.

“FRAMESHIFT” relates to an insertion or a deletion. If the frameshift occurs in a coding region, the Table provides the translation of the frameshifted codons 3' to the polymorphic site.

10 “Protein classification of CuraGen gene” provides a generic class into which the protein is classified. During the course of the work leading to the filing of this application, several classes of proteins were identified. Some are described further below.

15 “Name of protein identified following a BLASTX analysis of the CuraGen sequence” provides the database reference for the protein found to resemble the novel reference-polymorphism cognate pair most closely.

20 “Similarity (pvalue) following a BLASTX analysis” provides the pvalue, a statistical measure from the BLASTX analysis that the polymorphic sequence is similar to, and therefore an allele of, the reference, or wild-type, sequence. In the present application, a cutoff of $pvalue > 1 \times 10^{-50}$ (entered, for example, as 1.0E-50 in the Table) is used to establish that the reference-polymorphic cognate pairs are novel. A $pvalue < 1 \times 10^{-50}$ defines proteins considered to be already known.

“Map location” provides any information available at the time of filing related to localization of a gene on a chromosome.

25 The polymorphisms are arranged in the Table in the following order.

SEQ ID NOs: 1-722 are SNPs that are silent.

SEQ ID NOs: 723-797 are SNPs that lead to conservative amino acid changes.

SEQ ID NOs: 798-989 are SNPs that lead to nonconservative amino acid changes.

5 SEQ ID NOs: 990-1095 are SNPs that involve a gap. With respect to the reference or wild-type sequence at the position of the polymorphism, the allelic cSNP introduces an additional nucleotide (an insertion) or deletes a nucleotide (a deletion). An SNP that involves a gap generates a frame shift.

10 SEQ ID NOs: 1096-1170 are the amino acid sequences centered at the polymorphic amino acid residue for the protein products provided by SNPs that lead to conservative amino acid changes. These amino acid SEQ ID NOs: are derived from the corresponding nucleotide SEQ ID NOs: 723-797. 7 or 8 amino acids on either side of the polymorphic site are shown. The order in which these sequences appear mirrors the order of presentation of the cognate nucleotide sequences, and is set forth in the Table.

15 SEQ ID NOs: 1171-1362 are the amino acid sequences centered at the polymorphic amino acid residue for the protein products provided by SNPs that lead to nonconservative amino acid changes. These amino acid SEQ ID NOs: are derived from the corresponding nucleotide SEQ ID NOs: 798-989. 7 or 8 amino acids on either side of the polymorphic site are shown. The order in which these sequences appear mirrors the
20 order of presentation of the cognate nucleotide sequences, and is set forth in the Table.

SEQ ID NOs: 1363-1468 are the amino acid sequences centered at the polymorphic amino acid residue for the protein products provided by SNPs that lead to frameshift-induced amino acid changes. These amino acid SEQ ID NOs: are derived from the corresponding nucleotide SEQ ID NOs: 990-1095. 7 or 8 amino acids on either
25 side of the polymorphic site are shown. The order in which these sequences appear mirrors the order of presentation of the cognate nucleotide sequences, and is set forth in the Table.

Provided herein are compositions which include, or are capable of detecting, nucleic acid sequences having these polymorphisms, as well as methods of using nucleic acids.

IDENTIFICATION OF INDIVIDUALS CARRYING SNPs

5 Individuals carrying polymorphic alleles of the invention may be detected at either the DNA, the RNA, or the protein level using a variety of techniques that are well known in the art. Strategies for identification and detection are described in *e.g.*, EP 730,663, EP 717,113, and PCT US97/02102. The present methods usually employ pre-characterized polymorphisms. That is, the genotyping location and nature of
10 polymorphic forms present at a site have already been determined. The availability of this information allows sets of probes to be designed for specific identification of the known polymorphic forms.

Many of the methods described below require amplification of DNA from target samples. This can be accomplished by *e.g.*, PCR. See generally PCR Technology:
15 Principles and Applications for DNA Amplification (ed. H.A. Erlich, Freeman Press, NY, NY, 1992); PCR Protocols: A Guide to Methods and Applications (eds. Innis, et al., Academic Press, San Diego, CA, 1990); Mattila et al., Nucleic Acids Res. 19, 4967 (1991); Eckert et al., PCR Methods and Applications 1, 17 (1991); PCR (eds. McPherson et al., IRL Press, Oxford); and U.S. Patent 4,683,202.

20 The phrase "recombinant protein" or "recombinantly produced protein" refers to a peptide or protein produced using non-native cells that do not have an endogenous copy of DNA able to express the protein. In particular, as used herein, a recombinantly produced protein relates to the gene product of a polymorphic allele, *i.e.*, a "polymorphic protein" containing an altered amino acid at the site of translation of the nucleotide
25 polymorphism. The cells produce the protein because they have been genetically altered by the introduction of the appropriate nucleic acid sequence. The recombinant protein will not be found in association with proteins and other subcellular components normally associated with the cells producing the protein. The terms "protein" and "polypeptide" are used interchangeably herein.

The phrase "substantially purified" or "isolated" when referring to a nucleic acid, peptide or protein, means that the chemical composition is in a milieu containing fewer, or preferably, essentially none, of other cellular components with which it is naturally associated. Thus, the phrase "isolated" or "substantially pure" refers to nucleic acid preparations that lack at least one protein or nucleic acid normally associated with the nucleic acid in a host cell. It is preferably in a homogeneous state although it can be in either a dry or aqueous solution. Purity and homogeneity are typically determined using analytical chemistry techniques such as gel electrophoresis or high performance liquid chromatography. Generally, a substantially purified or isolated nucleic acid or protein will comprise more than 80% of all macromolecular species present in the preparation. Preferably, the nucleic acid or protein is purified to represent greater than 90% of all macromolecular species present. More preferably the nucleic acid or protein is purified to greater than 95%, and most preferably the nucleic acid or protein is purified to essential homogeneity, wherein other macromolecular species are not detected by conventional analytical procedures.

The genomic DNA used for the diagnosis may be obtained from any nucleated cells of the body, such as those present in peripheral blood, urine, saliva, buccal samples, surgical specimen, and autopsy specimens. The DNA may be used directly or may be amplified enzymatically in vitro through use of PCR (Saiki et al. Science 239:487-491 (1988)) or other in vitro amplification methods such as the ligase chain reaction (LCR) (Wu and Wallace Genomics 4:560-569 (1989)), strand displacement amplification (SDA) (Walker et al. Proc. Natl. Acad. Sci. U.S.A. 89:392-396 (1992)), self-sustained sequence replication (3SR) (Fahy et al. PCR Methods P&J 1:25-33 (1992)), prior to mutation analysis.

The method for preparing nucleic acids in a form that is suitable for mutation detection is well known in the art. A "nucleic acid" is a deoxyribonucleotide or ribonucleotide polymer in either single-or double-stranded form, including known analogs of natural nucleotides unless otherwise indicated. The term "nucleic acids", as used herein, refers to either DNA or RNA. "Nucleic acid sequence" or "polynucleotide sequence" refers to a single-stranded sequence of deoxyribonucleotide or ribonucleotide

bases read from the 5' end to the 3' end. The direction of 5' to 3' addition of nascent RNA transcripts is referred to as the transcription direction; sequence regions on the DNA strand having the same sequence as the RNA and which are beyond the 5' end of the RNA transcript in the 5' direction are referred to as "upstream sequences"; sequence regions on the DNA strand having the same sequence as the RNA and which are beyond the 3' end of the RNA transcript in the 3' direction are referred to as "downstream sequences". The term includes both self-replicating plasmids, infectious polymers of DNA or RNA and nonfunctional DNA or RNA. The complement of any nucleic acid sequence of the invention is understood to be included in the definition of that sequence. "Nucleic acid probes" may be DNA or RNA fragments.

The detection of polymorphisms in specific DNA sequences, can be accomplished by a variety of methods including, but not limited to, restriction-fragment-length-polymorphism detection based on allele-specific restriction-endonuclease cleavage (Kan and Dozy Lancet ii:910-912 (1978)), hybridization with allele-specific oligonucleotide probes (Wallace et al. Nucl. Acids Res. 6:3543-3557 (1978)), including immobilized oligonucleotides (Saiki et al. Proc. Natl. Acad. Sci. USA, 86:6230-6234 (1969)) or oligonucleotide arrays (Maskos and Southern Nucl. Acids Res 21:2269-2270 (1993)), allele-specific PCR (Newton et al. Nucl Acids Res 17:2503-2516 (1989)), mismatch-repair detection (MRD) (Faham and Cox Genome Res 5:474-482 (1995)), binding of MutS protein (Wagner et al. Nucl Acids Res 23:3944-3948 (1995)), denaturing-gradient gel electrophoresis (DGGE) (Fisher and Lerman et al. Proc. Natl. Acad. Sci. U.S.A. 80:1579-1583 (1983)), single-strand-conformation-polymorphism detection (Orita et al. Genomics 5:874-879 (1983)), RNAase cleavage at mismatched base-pairs (Myers et al. Science 230:1242 (1985)), chemical (Cotton et al. Proc. Natl. w Sci. U.S.A., 82:4397-4401 (1988)) or enzymatic (Youil et al. Proc. Natl. Acad. Sci. U.S.A. 92:87-91 (1995)) cleavage of heteroduplex DNA, methods based on allele specific primer extension (Syvanen et al. Genomics 8:684-692 (1990)), genetic bit analysis (GBA) (Nikiforov et al. &&I Acids 22:4167-4175 (1994)), the oligonucleotide-ligation assay (OLA) (Landegren et al. Science 241:1077 (1988)), the allele-specific ligation chain reaction (LCR) (Barrany Proc. Natl. Acad. Sci. U.S.A. 88:189-193 (1991)), gap-LCR (Abravaya et al. Nucl Acids Res 23:675-682 (1995)), radioactive and/or fluorescent

DNA sequencing using standard procedures well known in the art, and peptide nucleic acid (PNA) assays (Orum et al., *Nucl. Acids Res.* 21:5332-5356 (1993); Thiede et al., *Nucl. Acids Res.* 24:983-984 (1996)).

“Specific hybridization” or “selective hybridization” refers to the binding, or duplexing, of a nucleic acid molecule only to a second particular nucleotide sequence to which the nucleic acid is complementary, under suitably stringent conditions when that sequence is present in a complex mixture (e.g., total cellular DNA or RNA). “Stringent conditions” are conditions under which a probe will hybridize to its target subsequence, but to no other sequences. Stringent conditions are sequence-dependent and are different in different circumstances. Longer sequences hybridize specifically at higher temperatures than shorter ones. Generally, stringent conditions are selected such that the temperature is about 5°C lower than the thermal melting point (T_m) for the specific sequence to which hybridization is intended to occur at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic acid concentration) at which 50% of the target sequence hybridizes to the complementary probe at equilibrium. Typically, stringent conditions include a salt concentration of at least about 0.01 to about 1.0 M Na ion concentration (or other salts), at pH 7.0 to 8.3. The temperature is at least about 30°C for short probes (e.g., 10 to 50 nucleotides). Stringent conditions can also be achieved with the addition of destabilizing agents such as formamide. For example, conditions of 5X SSPE (750 mM NaCl, 50 mM NaPhosphate, 5 mM EDTA, pH 7.4) and a temperature of 25-30°C are suitable for allele-specific probe hybridization.

“Complementary” or “target” nucleic acid sequences refer to those nucleic acid sequences which selectively hybridize to a nucleic acid probe. Proper annealing conditions depend, for example, upon a probe’s length, base composition, and the number of mismatches and their position on the probe, and must often be determined empirically. For discussions of nucleic acid probe design and annealing conditions, see, for example, Sambrook et al., or *Current Protocols in Molecular Biology*, F. Ausubel et al., ed., Greene Publishing and Wiley-Interscience, New York (1987).

A perfectly matched probe has a sequence perfectly complementary to a particular target sequence. The test probe is typically perfectly complementary to a portion of the target sequence. A "polymorphic" marker or site is the locus at which a sequence difference occurs with respect to a reference sequence. Polymorphic markers include restriction fragment length polymorphisms, variable number of tandem repeats (VNTR's), hypervariable regions, minisatellites, dinucleotide repeats, trinucleotide repeats, tetranucleotide repeats, simple sequence repeats, and insertion elements such as Alu. The reference allelic form may be, for example, the most abundant form in a population, or the first allelic form to be identified, and other allelic forms are designated as alternative, variant or polymorphic alleles. The allelic form occurring most frequently in a selected population is sometimes referred to as the "wild type" form, and herein may also be referred to as the "reference" form. Diploid organisms may be homozygous or heterozygous for allelic forms. A diallelic polymorphism has two distinguishable forms (i.e., base sequences), and a triallelic polymorphism has three such forms.

As used herein an "oligonucleotide" is a single-stranded nucleic acid ranging in length from 2 to about 60 bases. Oligonucleotides are often synthetic but can also be produced from naturally occurring polynucleotides. A probe is an oligonucleotide capable of binding to a target nucleic acid of a complementary sequence through one or more types of chemical bonds, usually through complementary base pairing via hydrogen bond formation. Oligonucleotide probes are often between 5 and 60 bases, and, in specific embodiments, may be between 10-40, or 15-30 bases long. An oligonucleotide probe may include natural (i.e. A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in an oligonucleotide probe may be joined by a linkage other than a phosphodiester bond, such as a phosphoramidite linkage or a phosphorothioate linkage, or they may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than by phosphodiester bonds, so long as it does not interfere with hybridization.

As used herein, the term "primer" refers to a single-stranded oligonucleotide which acts as a point of initiation of template-directed DNA synthesis under appropriate conditions (e.g., in the presence of four different nucleoside triphosphates and a

polymerization agent, such as DNA polymerase, RNA polymerase or reverse transcriptase) in an appropriate buffer and at a suitable temperature. The appropriate length of a primer depends on the intended use of the primer, but typically ranges from 15 to 30 nucleotides. Short primer molecules generally require cooler temperatures to form sufficiently stable hybrid complexes with the template. A primer need not be perfectly complementary to the exact sequence of the template, but should be sufficiently complementary to hybridize with it. The term "primer site" refers to the sequence of the target DNA to which a primer hybridizes. The term "primer pair" refers to a set of primers including a 5' (upstream) primer that hybridizes with the 5' end of the DNA sequence to be amplified and a 3' (downstream) primer that hybridizes with the complement of the 3' end of the sequence to be amplified.

DNA fragments can be prepared, for example, by digesting plasmid DNA, or by use of PCR. Oligonucleotides for use as primers or probes are chemically synthesized by methods known in the field of the chemical synthesis of polynucleotides, including by way of non-limiting example the phosphoramidite method described by Beaucage and Carruthers, Tetrahedron Lett 22:1859-1 862 (1981) and the triester method provided by Matteucci, et al., J. Am. Chem. Soc., 103:3185 (1981) both incorporated herein by reference. These syntheses may employ an automated synthesizer, as described in Needham-VanDevanter, D.R., et al., Nucleic Acids Res. 12:61596168 (1984).

Purification of oligonucleotides may be carried out by either native acrylamide gel electrophoresis or by anion-exchange HPLC as described in Pearson, J.D. and Regnier, F.E., J. Chrom., 255:137-149 (1983). A double stranded fragment may then be obtained, if desired, by annealing appropriate complementary single strands together under suitable conditions or by synthesizing the complementary strand using a DNA polymerase with an appropriate primer sequence. Where a specific sequence for a nucleic acid probe is given, it is understood that the complementary strand is also identified and included. The complementary strand will work equally well in situations where the target is a double-stranded nucleic acid.

The sequence of the synthetic oligonucleotide or of any nucleic acid fragment can be can be obtained using either the dideoxy chain termination method or the Maxam-

Gilbert method (see Sambrook et al. Molecular Cloning - a Laboratory Manual (2nd Ed.), Vols. 1-3, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, (1989), which is incorporated herein by reference. This manual is hereinafter referred to as "Sambrook et al." ; Zyskind et al., (1988)). Recombinant DNA Laboratory Manual, (Acad. Press, New York). Oligonucleotides useful in diagnostic assays are typically at least 8 consecutive nucleotides in length, and may range upwards of 18 nucleotides in length to greater than 100 or more consecutive nucleotides.

Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the SNP-containing nucleotide sequences of the invention, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, about 25, about 50, or about 60 nucleotides or an entire SNP coding strand, or to only a portion thereof.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a polymorphic nucleotide sequence of the invention. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid. In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence of the invention. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences disclosed herein, antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. For example, the antisense nucleic acid molecule can generally be complementary to the entire coding region of an mRNA, but more preferably as

embodied herein, it is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of the mRNA. An antisense oligonucleotide can range in length between about 5 and about 60 nucleotides, preferably between about 10 and about 45 nucleotides, more preferably between about 15 and 40 nucleotides, and still more preferably between about 15 and 30 in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following section).

The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a polymorphic protein to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementary to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res* 15: 6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res* 15: 6131-6148) or a chimeric RNA-DNA analogue (Inoue *et al.* (1987) *FEBS Lett* 215: 327-330).

The following terms are used to describe the sequence relationships between two or more nucleic acids or polynucleotides: "reference sequence", "comparison window", "sequence identity", "percentage of sequence identity", and "substantial identity". A "reference sequence" is a defined sequence used as a basis for a sequence comparison; a reference sequence may be a subset of a larger sequence, for example, as a segment of a full-length cDNA or gene sequence given in a sequence listing, or may comprise a

complete cDNA or gene sequence. Optimal alignment of sequences for aligning a comparison window may, for example, be conducted by the local homology algorithm of Smith and Waterman Adv. Appl. Math. 2482 (1981), by the homology alignment algorithm of Needleman and Wunsch J. Mol. Biol. 48:443 (1970), by the search for similarity method of Pearson and Lipman Proc. Natl. Acad. Sci. U.S.A. 852444 (1988), or by computerized implementations of these algorithms (for example, GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package Release 7.0, Genetics Computer Group, 575 Science Dr., Madison, WI).

Techniques for nucleic acid manipulation of the nucleic acid sequences harboring the cSNP's of the invention, such as subcloning nucleic acid sequences encoding polypeptides into expression vectors, labeling probes, DNA hybridization, and the like, are described generally in Sambrook et al., The phrase "nucleic acid sequence encoding" refers to a nucleic acid which directs the expression of a specific protein, peptide or amino acid sequence. The nucleic acid sequences include both the DNA strand sequence that is transcribed into RNA and the RNA sequence that is translated into protein, peptide or amino acid sequence. The nucleic acid sequences include both the full length nucleic acid sequences disclosed herein as well as non-full length sequences derived from the full length protein. It being further understood that the sequence includes the degenerate codons of the native sequence or sequences which may be introduced to provide codon preference in a specific host cell. Consequently, the principles of probe selection and array design can readily be extended to analyze more complex polymorphisms (see EP 730,663). For example, to characterize a triallelic SNP polymorphism, three groups of probes can be designed tiled on the three polymorphic forms as described above. As a further example, to analyze a diallelic polymorphism involving a deletion of a nucleotide, one can tile a first group of probes based on the undeleted polymorphic form as the reference sequence and a second group of probes based on the deleted form as the reference sequence.

For assay of genomic DNA, virtually any biological convenient tissue sample can be used. Suitable samples include whole blood, semen, saliva, tears, urine, fecal material, sweat, buccal, skin and hair can be used. Genomic DNA is typically amplified before

analysis. Amplification is usually effected by PCR using primers flanking a suitable fragment e.g., of 50-500 nucleotides containing the locus of the polymorphism to be analyzed. Target is usually labeled in the course of amplification. The amplification product can be RNA or DNA, single stranded or double stranded. If double stranded, the amplification product is typically denatured before application to an array. If genomic DNA is analyzed without amplification, it may be desirable to remove RNA from the sample before applying it to the array. Such can be accomplished by digestion with DNase-free RNase.

DETECTION OF POLYMORPHISMS IN A NUCLEIC ACID SAMPLE

The SNPs disclosed herein can be used to determine which forms of a characterized polymorphism are present in individuals under analysis.

The design and use of allele-specific probes for analyzing polymorphisms is described by e.g., Saiki et al., Nature 324, 163-166 (1986); Dattagupta, EP 235,726, Saiki, WO 89/11548. Allele-specific probes can be designed that hybridize to a segment of target DNA from one individual but do not hybridize to the corresponding segment from another individual due to the presence of different polymorphic forms in the respective segments from the two individuals. Hybridization conditions should be sufficiently stringent that there is a significant difference in hybridization intensity between alleles, and preferably an essentially binary response, whereby a probe hybridizes to only one of the alleles. Some probes are designed to hybridize to a segment of target DNA such that the polymorphic site aligns with a central position (e.g., in a 15-mer at the 7 position; in a 16-mer, at either the 7, 8 or 9 position) of the probe. This design of probe achieves good discrimination in hybridization between different allelic forms.

Allele-specific probes are often used in pairs, one member of a pair showing a perfect match to a reference form of a target sequence and the other member showing a perfect match to a variant form. Several pairs of probes can then be immobilized on the same support for simultaneous analysis of multiple polymorphisms within the same target sequence.

The polymorphisms can also be identified by hybridization to nucleic acid arrays, some examples of which are described in published PCT application WO 95/11995. WO 95/11995 also describes subarrays that are optimized for detection of a variant form of a precharacterized polymorphism. Such a subarray contains probes designed to be complementary to a second reference sequence, which is an allelic variant of the first reference sequence. The second group of probes is designed by the same principles, except that the probes exhibit complementarity to the second reference sequence. The inclusion of a second group (or further groups) can be particularly useful for analyzing short subsequences of the primary reference sequence in which multiple mutations are expected to occur within a short distance commensurate with the length of the probes (e.g., two or more mutations within 9 to 21 bases).

An allele-specific primer hybridizes to a site on a target DNA overlapping a polymorphism and only primes amplification of an allelic form to which the primer exhibits perfect complementarity. See Gibbs, Nucleic Acid Res. 17 2427-2448 (1989). This primer is used in conjunction with a second primer which hybridizes at a distal site. Amplification proceeds from the two-primers, resulting in a detectable product which indicates the particular allelic form is present. A control is usually performed with a second pair of primers, one of which shows a single base mismatch at the polymorphic site and the other of which exhibits perfect complementarity to a distal site. The single-base mismatch prevents amplification and no detectable product is formed. The method works best when the mismatch is included in the 3'-most position of the oligonucleotide aligned with the polymorphism because this position is most destabilizing to elongation from the primer (see, e.g., WO 93/22456).

Amplification products generated using the polymerase chain reaction can be analyzed by the use of denaturing gradient gel electrophoresis. Different alleles can be identified based on the different sequence-dependent melting properties and electrophoretic migration of DNA in solution. Erlich, ed., PCR Technology, Principles and Applications for DNA Amplification, (W.H. Freeman and Co New York, 1992, Chapter 7).

Alleles of target sequences can be differentiated using single-strand conformation polymorphism analysis, which identifies base differences by alteration in electrophoretic migration of single stranded PCR products, as described in Orita et al., Proc. Nat. Acad. Sci. 86, 2766-2770 (1989). Amplified PCR products can be generated and heated or otherwise denatured, to form single stranded amplification products. Single-stranded nucleic acids may refold or form secondary structures which are partially dependent on the base sequence. The different electrophoretic mobilities of single-stranded amplification products can be related to base-sequence differences between alleles of target sequences.

The genotype of an individual with respect to a pathology suspected of being caused by a genetic polymorphism may be assessed by association analysis. Phenotypic traits suitable for association analysis include diseases that have known but hitherto unmapped genetic components (e.g., agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary hemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria).

Phenotypic traits also include symptoms of, or susceptibility to, multifactorial diseases of which a component is or may be genetic, such as autoimmune diseases, inflammation, cancer, system, diseases of the nervous and infection by pathogenic microorganisms. Some examples of autoimmune diseases include rheumatoid arthritis, multiple sclerosis, diabetes (insulin-dependent and non-independent), systemic lupus erythematosus and Graves disease. Some examples of cancers include cancers of the bladder, brain, breast, colon, esophagus, kidney, oral cavity, ovary, pancreas, prostate, skin, stomach, leukemia, liver, lung, and uterus. Phenotypic traits also include characteristics such as longevity, appearance (e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments.

Determination of which polymorphic forms occupy a set of polymorphic sites in an individual identifies a set of polymorphic forms that distinguishes the individual. See generally National Research Council, *The Evaluation of Forensic DNA Evidence* (Eds. Pollard et al., National Academy Press, DC, 1996). Since the polymorphic sites are within a 50,000 bp region in the human genome, the probability of recombination between these polymorphic sites is low. That low probability means the haplotype (the set of all 10 polymorphic sites) set forth in this application should be inherited without change for at least several generations. The more sites that are analyzed the lower the probability that the set of polymorphic forms in one individual is the same as that in an unrelated individual. Preferably, if multiple sites are analyzed, the sites are unlinked. Thus, polymorphisms of the invention are often used in conjunction with polymorphisms in distal genes. Preferred polymorphisms for use in forensics are diallelic because the population frequencies of two polymorphic forms can usually be determined with greater accuracy than those of multiple polymorphic forms at multi-allelic loci.

The capacity to identify a distinguishing or unique set of forensic markers in an individual is useful for forensic analysis. For example, one can determine whether a blood sample from a suspect matches a blood or other tissue sample from a crime scene by determining whether the set of polymorphic forms occupying selected polymorphic sites is the same in the suspect and the sample. If the set of polymorphic markers does not match between a suspect and a sample, it can be concluded (barring experimental error) that the suspect was not the source of the sample. If the set of markers does match, one can conclude that the DNA from the suspect is consistent with that found at the crime scene. If frequencies of the polymorphic forms at the loci tested have been determined (e.g., by analysis of a suitable population of individuals), one can perform a statistical analysis to determine the probability that a match of suspect and crime scene sample would occur by chance.

$p(\text{ID})$ is the probability that two random individuals have the same polymorphic or allelic form at a given polymorphic site. In diallelic loci, four genotypes are possible: AA, AB, BA, and BB. If alleles A and B occur in a haploid genome of the organism with frequencies x and y , the probability of each genotype in a diploid organism are (see WO

95/12607):

$$\text{Homozygote: } p(AA)=x^2$$

$$\text{Homozygote: } p(BB)=y^2=(1-x)^2$$

$$\text{Single Heterozygote: } p(AB)=p(BA)=xy=x(1-x)$$

5 Both Heterozygotes: $p(AB + BA)=2xy=2x(1-x)$

The probability of identity at one locus (i.e, the probability that two individuals, picked at random from a population will have identical polymorphic forms at a given locus) is given by the equation:

$$p(ID)=(x^2)^2 + (2xy)^2 + (y^2)^2.$$

10 These calculations can be extended for any number of polymorphic forms at a given locus. For example, the probability of identity $p(ID)$ for a 3-allele system where the alleles have the frequencies in the population of x , y and z , respectively, is equal to the sum of the squares of the genotype frequencies:

$$p(ID)=x^4 + (2xy)^2 + (2yz)^2 + (2xz)^2 + y^4 + z^4$$

15 In a locus of n alleles, the appropriate binomial expansion is used to calculate $p(ID)$ and $p(exc)$.

The cumulative probability of identity ($\text{cum } p(ID)$) for each of multiple unlinked loci is determined by multiplying the probabilities provided by each locus:

$$\text{cum } p(ID)=p(ID1)p(ID2)p(ID3) \dots p(IDn)$$

20 The cumulative probability of non-identity for n loci (i.e. the probability that two random individuals will be different at 1 or more loci) is given by the equation:

$$\text{cum } p(nonID)=1-\text{cum } p(ID).$$

If several polymorphic loci are tested, the cumulative probability of non-identity for random individuals becomes very high (e.g., one billion to one). Such probabilities can be taken into account together with other evidence in determining the guilt or innocence of the suspect.

5 The object of paternity testing is usually to determine whether a male is the father of a child. In most cases, the mother of the child is known and thus, the mother's contribution to the child's genotype can be traced. Paternity testing investigates whether the part of the child's genotype not attributable to the mother is consistent with that of the putative father. Paternity testing can be performed by analyzing sets of polymorphisms in
10 the putative father and the child.

 If the set of polymorphisms in the child attributable to the father does not match the putative father, it can be concluded, barring experimental error, that the putative father is not the real father. If the set of polymorphisms in the child attributable to the father does match the set of polymorphisms of the putative father, a statistical calculation
15 can be performed to determine the probability of coincidental match.

 The probability of parentage exclusion (representing the probability that a random male will have a polymorphic form at a given polymorphic site that makes him incompatible as the father) is given by the equation (see WO 95/12607):

$$p(exc)=xy(1-xy)$$

20 where x and y are the population frequencies of alleles A and B of a diallelic polymorphic site. (At a triallelic site $p(exc)=xy(1-xy)+yz(1-yz)+xz(1-xz)+3xyz(1-xyz)$), where x, y and z are the respective population frequencies of alleles A, B and C). The probability of non-exclusion is:

$$p(non-exc)=1-p(exc)$$

25 The cumulative probability of non-exclusion (representing the value obtained when n loci are used) is thus:

$$cum\ p(non-exc)=p(non-exc1)p(non-exc2)p(non-exc3)\dots p(non-exc_n)$$

The cumulative probability of exclusion for n loci (representing the probability that a random male will be excluded) is:

$$\text{cum } p(\text{exc}) = 1 - \text{cum } p(\text{non-exc}).$$

If several polymorphic loci are included in the analysis, the cumulative probability of exclusion of a random male is very high. This probability can be taken into account in assessing the liability of a putative father whose polymorphic marker set matches the child's polymorphic marker set attributable to his/her father.

The polymorphisms of the invention may contribute to the phenotype of an organism in different ways. Some polymorphisms occur within a protein coding sequence and contribute to phenotype by affecting protein structure. The effect may be neutral, beneficial or detrimental, or both beneficial and detrimental, depending on the circumstances. For example, a heterozygous sickle cell mutation confers resistance to malaria, but a homozygous sickle cell mutation is usually lethal. Other polymorphisms occur in noncoding regions but may exert phenotypic effects indirectly via influence on replication, transcription, and translation. A single polymorphism may affect more than one phenotypic trait. Likewise, a single phenotypic trait may be affected by polymorphisms in different genes. Further, some polymorphisms predispose an individual to a distinct mutation that is causally related to a certain phenotype.

Phenotypic traits include diseases that have known but hitherto unmapped genetic components. Phenotypic traits also include symptoms of, or susceptibility to, multifactorial diseases of which a component is or may be genetic, such as autoimmune diseases, inflammation, cancer, diseases of the nervous system, and infection by pathogenic microorganisms. Some examples of autoimmune diseases include rheumatoid arthritis, multiple sclerosis, diabetes (insulin-dependent and non-independent), systemic lupus erythematosus and Graves disease. Some examples of cancers include cancers of the bladder, brain, breast, colon, esophagus, kidney, leukemia, liver, lung, oral cavity, ovary, pancreas, prostate, skin, stomach and uterus. Phenotypic traits also include characteristics such as longevity, appearance (e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic

treatments.

Correlation is performed for a population of individuals who have been tested for the presence or absence of a phenotypic trait of interest and for polymorphic marker sets. To perform such analysis, the presence or absence of a set of polymorphisms (i.e. a polymorphic set) is determined for a set of the individuals, some of whom exhibit a particular trait, and some of whom exhibit lack of the trait. The alleles of each polymorphism of the set are then reviewed to determine whether the presence or absence of a particular allele is associated with the trait of interest. Correlation can be performed by standard statistical methods and statistically significant correlations between polymorphic form(s) and phenotypic characteristics are noted. For example, it might be found that the presence of allele A1 at polymorphism A correlates with heart disease. As a further example, it might be found that the combined presence of allele A1 at polymorphism A and allele B1 at polymorphism B correlates with increased milk production of a farm animal.

Such correlations can be exploited in several ways. In the case of a strong correlation between a set of one or more polymorphic forms and a disease for which treatment is available, detection of the polymorphic form set in a human or animal patient may justify immediate administration of treatment, or at least the institution of regular monitoring of the patient. Detection of a polymorphic form correlated with serious disease in a couple contemplating a family may also be valuable to the couple in their reproductive decisions. For example, the female partner might elect to undergo in vitro fertilization to avoid the possibility of transmitting such a polymorphism from her husband to her offspring. In the case of a weaker, but still statistically significant correlation between a polymorphic set and human disease, immediate therapeutic intervention or monitoring may not be justified. Nevertheless, the patient can be motivated to begin simple life-style changes (e.g., diet, exercise) that can be accomplished at little cost to the patient but confer potential benefits in reducing the risk of conditions to which the patient may have increased susceptibility by virtue of variant alleles. Identification of a polymorphic set in a patient correlated with enhanced receptiveness to one of several treatment regimes for a disease indicates that this

treatment regime should be followed.

For animals and plants, correlations between characteristics and phenotype are useful for breeding for desired characteristics. For example, Beitz et al., U.S. Pat. No. 5,292,639 discuss use of bovine mitochondrial polymorphisms in a breeding program to improve milk production in cows. To evaluate the effect of mtDNA D-loop sequence polymorphism on milk production, each cow was assigned a value of 1 if variant or 0 if wild type with respect to a prototypical mitochondrial DNA sequence at each of 17 locations considered.

The previous section concerns identifying correlations between phenotypic traits and polymorphisms that directly or indirectly contribute to those traits. The present section describes identification of a physical linkage between a genetic locus associated with a trait of interest and polymorphic markers that are not associated with the trait, but are in physical proximity with the genetic locus responsible for the trait and co-segregate with it. Such analysis is useful for mapping a genetic locus associated with a phenotypic trait to a chromosomal position, and thereby cloning gene(s) responsible for the trait. See Lander et al., *Proc. Natl. Acad. Sci. (USA)* 83, 7353-7357 (1986); Lander et al., *Proc. Natl. Acad. Sci. (USA)* 84, 2363-2367 (1987); Donis-Keller et al., *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 185-199 (1989)). Genes localized by linkage can be cloned by a process known as directional cloning. See Wainwright, *Med. J. Australia* 159, 170-174 (1993); Collins, *Nature Genetics* 1, 3-6 (1992) (each of which is incorporated by reference in its entirety for all purposes).

Linkage studies are typically performed on members of a family. Available members of the family are characterized for the presence or absence of a phenotypic trait and for a set of polymorphic markers. The distribution of polymorphic markers in an informative meiosis is then analyzed to determine which polymorphic markers co-segregate with a phenotypic trait. See, e.g., Kerem et al., *Science* 245, 1073-1080 (1989); Monaco et al., *Nature* 316, 842 (1985); Yamoka et al., *Neurology* 40, 222-226 (1990); Rossiter et al., *FASEB Journal* 5, 21-27 (1991).

Linkage is analyzed by calculation of LOD (log of the odds) values. A lod value

is the relative likelihood of obtaining observed segregation data for a marker and a genetic locus when the two are located at a recombination fraction RF , versus the situation in which the two are not linked, and thus segregating independently (Thompson & Thompson, *Genetics in Medicine* (5th ed, W.B. Saunders Company, Philadelphia, 1991); Strachan, "Mapping the human genome" in *The Human Genome* (BIOS Scientific Publishers Ltd, Oxford), Chapter 4). A series of likelihood ratios are calculated at various recombination fractions (RF), ranging from $RF=0.0$ (coincident loci) to $RF=0.50$ (unlinked). Thus, the likelihood at a given value of RF is: probability of data if loci linked at RF to probability of data if loci unlinked. The computed likelihood is usually expressed as the \log_{10} of this ratio (i.e., a lod score). For example, a lod score of 3 indicates 1000:1 odds against an apparent observed linkage being a coincidence. The use of logarithms allows data collected from different families to be combined by simple addition. Computer programs are available for the calculation of lod scores for differing values of RF (e.g., LIPED, MLINK (Lathrop, *Proc. Nat. Acad. Sci. (USA)* 81, 3443-3446 (1984)). For any particular lod score, a recombination fraction may be determined from mathematical tables. See Smith et al., *Mathematical tables for research workers in human genetics* (Churchill, London, 1961); Smith, *Ann. Hum. Genet.* 32, 127-150 (1968). The value of RF at which the lod score is the highest is considered to be the best estimate of the recombination fraction.

Positive lod score values suggest that the two loci are linked, whereas negative values suggest that linkage is less likely (at that value of RF) than the possibility that the two loci are unlinked. By convention, a combined lod score of + 3 or greater (equivalent to greater than 1000:1 odds in favor of linkage) is considered definitive evidence that two loci are linked. Similarly, by convention, a negative lod score of -2 or less is taken as definitive evidence against linkage of the two loci being compared. Negative linkage data are useful in excluding a chromosome or a segment thereof from consideration. The search focuses on the remaining non-excluded chromosomal locations.

The invention further provides transgenic nonhuman animals capable of expressing an exogenous variant gene and/or having one or both alleles of an endogenous variant gene inactivated. Expression of an exogenous variant gene is usually achieved

by operably linking the gene to a promoter and optionally an enhancer, and microinjecting the construct into a zygote. See Hogan et al., "Manipulating the Mouse Embryo, A Laboratory Manual," Cold Spring Harbor Laboratory. (1989). Inactivation of endogenous variant genes can be achieved by forming a transgene in which a cloned variant gene is inactivated by insertion of a positive selection marker. See Capecchi, Science 244, 1288-1292 The transgene is then introduced into an embryonic stem cell, where it undergoes homologous recombination with an endogenous variant gene. Mice and other rodents are preferred animals. Such animals provide useful drug screening systems.

The invention further provides methods for assessing the pharmacogenomic susceptibility of a subject harboring a single nucleotide polymorphism to a particular pharmaceutical compound, or to a class of such compounds. Genetic polymorphism in drug-metabolizing enzymes, drug transporters, receptors for pharmaceutical agents, and other drug targets have been correlated with individual differences based on distinction in the efficacy and toxicity of the pharmaceutical agent administered to a subject. Pharmacogenomic characterization of a subjects susceptibility to a drug enhances the ability to tailor a dosing regimen to the particular genetic constitution of the subject, thereby enhancing and optimizing the therapeutic effectiveness of the therapy.

In cases in which a cSNP leads to a polymorphic protein that is ascribed to be the cause of a pathological condition, method of treating such a condition includes administering to a subject experiencing the pathology the wild type cognate of the polymorphic protein. Once administered in an effective dosing regimen, the wild type cognate provides complementation or remediation of the defect due to the polymorphic protein. The subject's condition is ameliorated by this protein therapy.

A subject suspected of suffering from a pathology ascribable to a polymorphic protein that arises from a cSNP is to be diagnosed using any of a variety of diagnostic methods capable of identifying the presence of the cSNP in the nucleic acid, or of the cognate polymorphic protein, in a suitable clinical sample taken from the subject. Once the presence of the cSNP has been ascertained, and the pathology is correctable by

administering a normal or wild-type gene, the subject is treated with a pharmaceutical composition that includes a nucleic acid that harbors the correcting wild-type gene, or a fragment containing a correcting sequence of the wild-type gene. Non-limiting examples of ways in which such a nucleic acid may be administered include incorporating the wild-type gene in a viral vector, such as an adenovirus or adeno associated virus, and administration of a naked DNA in a pharmaceutical composition that promotes intracellular uptake of the administered nucleic acid. Once the nucleic acid that includes the gene coding for the wild-type allele of the polymorphism is incorporated within a cell of the subject, it will initiate *de novo* biosynthesis of the wild-type gene product. If the nucleic acid is further incorporated into the genome of the subject, the treatment will have long-term effects, providing *de novo* synthesis of the wild-type protein for a prolonged duration. The synthesis of the wild-type protein in the cells of the subject will contribute to a therapeutic enhancement of the clinical condition of the subject.

A subject suffering from a pathology ascribed to a SNP may be treated so as to correct the genetic defect. (See Kren et al., Proc. Natl. Acad. Sci. USA 96:10349-10354 (1999)). Such a subject is identified by any method that can detect the polymorphism in a sample drawn from the subject. Such a genetic defect may be permanently corrected by administering to such a subject a nucleic acid fragment incorporating a repair sequence that supplies the wild-type nucleotide at the position of the SNP. This site-specific repair sequence encompasses an RNA/DNA oligonucleotide which operates to promote endogenous repair of a subject's genomic DNA. Upon administration in an appropriate vehicle, such as a complex with polyethylenimine or encapsulated in anionic liposomes, a genetic defect leading to an inborn pathology may be overcome, as the chimeric oligonucleotides induces incorporation of the wild-type sequence into the subject's genome. Upon incorporation, the wild-type gene product is expressed, and the replacement is propagated, thereby engendering a permanent repair.

The invention further provides kits comprising at least one allele-specific oligonucleotide as described above. Often, the kits contain one or more pairs of allele-specific oligonucleotides hybridizing to different forms of a polymorphism. In some kits, the allele-specific oligonucleotides are provided immobilized to a substrate. For

example, the same substrate can comprise allele-specific oligonucleotide probes for detecting at least 10, 100, 1000 or all of the polymorphisms shown in the Table. Optional additional components of the kit include, for example, restriction enzymes, reverse-transcriptase or polymerase, the substrate nucleoside triphosphates, means used to label
5 (for example, an avidin-enzyme conjugate and enzyme substrate and chromogen if the label is biotin), and the appropriate buffers for reverse transcription, PCR, or hybridization reactions. Usually, the kit also contains instructions for carrying out the hybridizing methods.

Several aspects of the present invention rely on having available the polymorphic
10 proteins encoded by the nucleic acids comprising a SNP of the inventions. There are various methods of isolating these nucleic acid sequences. For example, DNA is isolated from a genomic or cDNA library using labeled oligonucleotide probes having sequences complementary to the sequences disclosed herein.

Such probes can be used directly in hybridization assays. Alternatively probes
15 can be designed for use in amplification techniques such as PCR.

To prepare a cDNA library, mRNA is isolated from tissue such as heart or pancreas, preferably a tissue wherein expression of the gene or gene family is likely to occur. cDNA is prepared from the mRNA and ligated into a recombinant vector. The vector is transfected into a recombinant host for propagation, screening and cloning.
20 Methods for making and screening cDNA libraries are well known, See Gubler, U. and Hoffman, B.J. Gene 25:263-269 (1983) and Sambrook et al.

For a genomic library, for example, the DNA is extracted from tissue and either mechanically sheared or enzymatically digested to yield fragments of about 12-20 kb. The fragments are then separated by gradient centrifugation from undesired sizes and are
25 constructed in bacteriophage lambda vectors. These vectors and phage are packaged *in vitro*, as described in Sambrook, et al. Recombinant phage are analyzed by plaque hybridization as described in Benton and Davis, Science 196:180-182 (1977). Colony hybridization is carried out as generally described in M. Grunstein et al. Proc. Natl. Acad. Sci. USA. 72:3961-3965 (1975). DNA of interest is identified in either cDNA or

genomic libraries by its ability to hybridize with nucleic acid probes, for example on Southern blots, and these DNA regions are isolated by standard methods familiar to those of skill in the art. See Sambrook, et al.

In PCR techniques, oligonucleotide primers complementary to the two 3' borders of the DNA region to be amplified are synthesized. The polymerase chain reaction is then carried out using the two primers. See PCR Protocols: a Guide to Methods and Applications (Innis, M, Gelfand, D., Sninsky, J. and White, T., eds.), Academic Press, San Diego (1990). Primers can be selected to amplify the entire regions encoding a full-length sequence of interest or to amplify smaller DNA segments as desired. PCR can be used in a variety of protocols to isolate cDNAs encoding a sequence of interest. In these protocols, appropriate primers and probes for amplifying DNA encoding a sequence of interest are generated from analysis of the DNA sequences listed herein. Once such regions are PCR-amplified, they can be sequenced and oligonucleotide probes can be prepared from the sequence.

Once DNA encoding a sequence comprising a cSNP is isolated and cloned, one can express the encoded polymorphic proteins in a variety of recombinantly engineered cells. It is expected that those of skill in the art are knowledgeable in the numerous expression systems available for expression of DNA encoding a sequence of interest. No attempt to describe in detail the various methods known for the expression of proteins in prokaryotes or eukaryotes is made here.

In brief summary, the expression of natural or synthetic nucleic acids encoding a sequence of interest will typically be achieved by operably linking the DNA or cDNA to a promoter (which is either constitutive or inducible), followed by incorporation into an expression vector. The vectors can be suitable for replication and integration in either prokaryotes or eukaryotes. Typical expression vectors contain initiation sequences, transcription and translation terminators, and promoters useful for regulation of the expression of a polynucleotide sequence of interest. To obtain high level expression of a cloned gene, it is desirable to construct expression plasmids which contain, at the minimum, a strong promoter to direct transcription, a ribosome binding site for

translational initiation, and a transcription/translation terminator. The expression vectors may also comprise generic expression cassettes containing at least one independent terminator sequence, sequences permitting replication of the plasmid in both eukaryotes and prokaryotes, i.e., shuttle vectors, and selection markers for both prokaryotic and eukaryotic systems. See Sambrook et al.

A variety of prokaryotic expression systems may be used to express the polymorphic proteins of the invention. Examples include *E. coli*, *Bacillus*, *Streptomyces*, and the like.

It is preferred to construct expression plasmids which contain, at the minimum, a strong promoter to direct transcription, a ribosome binding site for translational initiation, and a transcription/translation terminator. Examples of regulatory regions suitable for this purpose in *E. coli* are the promoter and operator region of the *E. coli* tryptophan biosynthetic pathway as described by Yanofsky, C., J. Bacterial. 158:1018-1024 (1984) and the leftward promoter of phage lambda as described by A, I. and Hagen, D., Ann. Rev. Genet. 14:399-445 (1980). The inclusion of selection markers in DNA vectors transformed in *E. coli* is also useful. Examples of such markers include genes specifying resistance to ampicillin, tetracycline, or chloramphenicol. See Sambrook et al. for details concerning selection markers for use in *E. coli*.

To enhance proper folding of the expressed recombinant protein, during purification from *E. coli*, the expressed protein may first be denatured and then renatured. This can be accomplished by solubilizing the bacterially produced proteins in a chaotropic agent such as guanidine HCl and reducing all the cysteine residues with a reducing agent such as beta-mercaptoethanol. The protein is then renatured, either by slow dialysis or by gel filtration. See U.S. Patent No. 4,511,503. Detection of the expressed antigen is achieved by methods known in the art as radioimmunoassay, or Western blotting techniques or immunoprecipitation. Purification from *E. coli* can be achieved following procedures such as those described in U.S. Patent No. 4,511,503.

Any of a variety of eukaryotic expression systems such as yeast, insect cell lines, bird, fish, and mammalian cells, may also be used to express a polymorphic protein of the

invention. As explained briefly below, a nucleotide sequence harboring a cSNP may be expressed in these eukaryotic systems. Synthesis of heterologous proteins in yeast is well known. Methods in Yeast Genetics, Sherman, F., et al., Cold Spring Harbor Laboratory, (1982) is a well recognized work describing the various methods available to produce the protein in yeast. Suitable vectors usually have expression control sequences, such as promoters, including 3-phosphoglycerate kinase or other glycolytic enzymes, and an origin of replication, termination sequences and the like as desired. For instance, suitable vectors are described in the literature (Botstein, et al., Gene 8:17-24 (1979); Broach, et al., Gene 8:121-133 (1979)).

Two procedures are used in transforming yeast cells. In one case, yeast cells are first converted into protoplasts using zymolyase, lyticase or glusulase, followed by addition of DNA and polyethylene glycol (PEG). The PEG-treated protoplasts are then regenerated in a 3% agar medium under selective conditions. Details of this procedure are given in the papers by J.D. Beggs, Nature (London) 275:104-109 (1978); and Hinnen, A., et al., Proc. Natl. Acad. Sci. USA, 75:1929-1933 (1978). The second procedure does not involve removal of the cell wall. Instead the cells are treated with lithium chloride or acetate and PEG and put on selective plates (Ito, H., et al., J. Bact, 153:163-168 (1983)) cells and applying standard protein isolation techniques to the lysates.

The purification process can be monitored by using Western blot techniques or radioimmunoassay or other standard techniques. The sequences encoding the proteins of the invention can also be ligated to various immunoassay expression vectors for use in transforming cell cultures of, for instance, mammalian, insect, bird or fish origin. Illustrative of cell cultures useful for the production of the polypeptides are mammalian cells. Mammalian cell systems often will be in the form of monolayers of cells although mammalian cell suspensions may also be used. A number of suitable host cell lines capable of expressing intact proteins have been developed in the art, and include the HEK293, BHK21, and CHO cell lines, and various human cells such as COS cell lines, HeLa cells, myeloma cell lines, Jurkat cells, etc. Expression vectors for these cells can include expression control sequences, such as an origin of replication, a promoter (e.g.,

the CMV promoter, a HSV *tk* promoter or *pgk* (phosphoglycerate kinase) promoter), an enhancer (Queen et al. Immunol. Rev. 89:49 (1986)) and necessary processing information sites, such as ribosome binding sites, RNA splice sites, polyadenylation sites (e.g., an SV40 large T Ag poly A addition site), and transcriptional terminator sequences.

5 Other animal cells are available, for instance, from the American Type Culture Collection Catalogue of Cell Lines and Hybridomas (7th edition, (1992)). Appropriate vectors for expressing the proteins of the invention in insect cells are usually derived from baculovirus. Insect cell lines include mosquito larvae, silkworm, armyworm, moth and *Drosophila* cell lines such as a Schneider cell line (See Schneider J. Embryol. Exp. Morphol., 27:353-365 (1987). As indicated above, the vector, e.g., a plasmid, which is used to transform the host cell, preferably contains DNA sequences to initiate transcription and sequences to control the translation of the protein. These sequences are referred to as expression control sequences. As with yeast, when higher animal host cells are employed, polyadenylation or transcription terminator sequences from known
10 mammalian genes need to be incorporated into the vector. An example of a terminator sequence is the polyadenylation sequence from the bovine growth hormone gene. Sequences for accurate splicing of the transcript may also be included. An example of a splicing sequence is the VP1 intron from SV40 (Sprague, J. et al., J. Virol. 45: 773-781 (1983)). Additionally, gene sequences to control replication in the host cell may be
15 Saveria-Campo, M., 1985, "Bovine Papilloma virus DNA a Eukaryotic Cloning Vector" in DNA Cloning Vol. II a Practical Approach Ed. D.M. Glover, IRL Press, Arlington, Virginia pp. 213-238. The host cells are competent or rendered competent for transformation by various means. There are several well-known methods of introducing DNA into animal cells. These include: calcium phosphate precipitation, fusion of the
20 recipient cells with bacterial protoplasts containing the DNA, treatment of the recipient cells with liposomes containing the DNA, DEAE dextran, electroporation and micro-injection of the DNA directly into the cells.

The transformed cells are cultured by means well known in the art (Biochemical Methods in Cell Culture and Virology, Kuchler, R.J., Dowden, Hutchinson and Ross,
30 Inc., (1977)). The expressed polypeptides are isolated from cells grown as suspensions or

as monolayers. The latter are recovered by well known mechanical, chemical or enzymatic means.

General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, Methods in Enzymology 185, 537-566 (1990). As defined herein "operably linked" refers to linkage of a promoter upstream from a DNA sequence such that the promoter mediates transcription of the DNA sequence. Specifically, "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the gene encoding the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression sequence. The term "vector", refers to viral expression systems, autonomous self-replicating circular DNA (plasmids), and includes both expression and nonexpression plasmids.

The term "gene" as used herein is intended to refer to a nucleic acid sequence which encodes a polypeptide. This definition includes various sequence polymorphisms, mutations, and/or sequence variants wherein such alterations do not affect the function of the gene product. The term "gene" is intended to include not only coding sequences but also regulatory regions such as promoters, enhancers, termination regions and similar untranslated nucleotide sequences. The term further includes all introns and other DNA sequences spliced from the mRNA transcript, along with variants resulting from alternative splice sites.

A number of types of cells may act as suitable host cells for expression of the protein. Mammalian host cells include, for example, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A43 1 cells, human Co10205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from in vitro culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL- 60, U937, HaK or Jurkat cells. Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains,

Candida or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, e.g., Invitrogen, San Diego, California, U.S.A. (the MaxBac© kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed." The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein.

The polymorphic protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein. The protein may also be produced by known conventional chemical synthesis. Methods for constructing the proteins of the present invention by synthetic means are known to those skilled in the art.

The polymorphic proteins produced by recombinant DNA technology may be purified by techniques commonly employed to isolate or purify recombinant proteins. Recombinantly produced proteins can be directly expressed or expressed as a fusion protein. The protein is then purified by a combination of cell lysis (e.g., sonication) and affinity chromatography. For fusion products, subsequent digestion of the fusion protein with an appropriate proteolytic enzyme releases the desired polypeptide. The polypeptides of this invention may be purified to substantial purity by standard

techniques well known in the art, including selective precipitation with such substances as ammonium sulfate, column chromatography, immunopurification methods, and others. See, for instance, R. Scopes, Protein Purification: Principles and Practice, Springer-Verlag: New York (1982), incorporated herein by reference. For example, in an
5 embodiment, antibodies may be raised to the proteins of the invention as described herein. Cell membranes are isolated from a cell line expressing the recombinant protein, the protein is extracted from the membranes and immunoprecipitated. The proteins may then be further purified by standard protein chemistry techniques as described above.

The resulting expressed protein may then be purified from such culture (i.e.,
10 from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-Toyopearl@ or Cibacrom blue 3GA Sepharose B; one or more steps involving hydrophobic interaction
15 chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography. Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX). Kits for expression and purification of such
20 fusion proteins are commercially available from New England BioLab (Beverly, MA), Pharmacia (Piscataway, NJ) and InVitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("Flag") is commercially available from Kodak (New Haven, CT). Finally, one or more reverse-phase high performance liquid chromatography (RP-
25 HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance
30 with the present invention as an "isolated protein."

The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin molecules, *i.e.*, molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen, such as polymorphic. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, F_{ab} and $F_{(ab)2}$ fragments, and an F_{ab} expression library. In a specific embodiment, antibodies to human polymorphic proteins are disclosed.

The phrase "specifically binds to", "immunospecifically binds to" or is "specifically immunoreactive with", an antibody when referring to a protein or peptide, refers to a binding reaction which is determinative of the presence of the protein in the presence of a heterogeneous population of proteins and other biological materials. Thus, for example, under designated immunoassay conditions, the specified antibodies bind to a particular protein and do not bind in a significant amount to other proteins present in the sample. Specific binding to an antibody under such conditions may require an antibody that is selected for its specificity for a particular protein. Of particular interest in the present invention is an antibody that binds immunospecifically to a polymorphic protein but not to its cognate wild type allelic protein, or vice versa. A variety of immunoassay formats may be used to select antibodies specifically immunoreactive with a particular protein. For example, solid-phase ELISA immunoassays are routinely used to select monoclonal antibodies specifically immunoreactive with a protein. See Harlow and Lane (1988) *Antibodies, a Laboratory Manual*, Cold Spring Harbor Publications, New York, for a description of immunoassay formats and conditions that can be used to determine specific immunoreactivity.

Polyclonal and/or monoclonal antibodies that immunospecifically bind to polymorphic gene products but not to the corresponding prototypical or "wild-type" gene products are also provided. Antibodies can be made by injecting mice or other animals with the variant gene product or synthetic peptide. Monoclonal antibodies are screened as are described, for example, in Harlow & Lane, *Antibodies, A Laboratory Manual*, Cold Spring Harbor Press, New York (1988); Goding, *Monoclonal antibodies, Principles and Practice* (2d ed.) Academic Press, New York (1986). Monoclonal antibodies are

tested for specific immunoreactivity with a variant gene product and lack of immunoreactivity to the corresponding prototypical gene product.

An isolated polymorphic protein, or a portion or fragment thereof, can be used as an immunogen to generate the antibody that binds the polymorphic protein using standard techniques for polyclonal and monoclonal antibody preparation. The full-length polymorphic protein can be used or, alternatively, the invention provides antigenic peptide fragments of polymorphic for use as immunogens. The antigenic peptide of a polymorphic protein of the invention comprises at least 8 amino acid residues of the amino acid sequence encompassing the polymorphic amino acid and encompasses an epitope of the polymorphic protein such that an antibody raised against the peptide forms a specific immune complex with the polymorphic protein. Preferably, the antigenic peptide comprises at least 10 amino acid residues, more preferably at least 15 amino acid residues, even more preferably at least 20 amino acid residues, and most preferably at least 30 amino acid residues. Preferred epitopes encompassed by the antigenic peptide are regions of polymorphic that are located on the surface of the protein, *e.g.*, hydrophilic regions.

For the production of polyclonal antibodies, various suitable host animals (*e.g.*, rabbit, goat, mouse or other mammal) may be immunized by injection with the polymorphic protein. An appropriate immunogenic preparation can contain, for example, recombinantly expressed polymorphic protein or a chemically synthesized polymorphic polypeptide. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (*e.g.*, aluminum hydroxide), surface active substances (*e.g.*, lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), human adjuvants such as *Bacille Calmette-Guerin* and *Corynebacterium parvum*, or similar immunostimulatory agents. If desired, the antibody molecules directed against polymorphic proteins can be isolated from the mammal (*e.g.*, from the blood) and further purified by well known techniques, such as protein A chromatography, to obtain the IgG fraction.

The term "monoclonal antibody" or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that originates from the clone of a singly hybridoma cell, and that contains only one type of antigen binding site capable of immunoreacting with a particular epitope of a polymorphic protein. A monoclonal antibody composition thus typically displays a single binding affinity for a particular polymorphic protein with which it immunoreacts. For preparation of monoclonal antibodies directed towards a particular polymorphic protein, or derivatives, fragments, analogs or homologs thereof, any technique that provides for the production of antibody molecules by continuous cell line culture may be utilized. Such techniques include, but are not limited to, the hybridoma technique (see Kohler & Milstein, 1975 *Nature* 256: 495-497); the trioma technique; the human B-cell hybridoma technique (see Kozbor, *et al.*, 1983 *Immunol Today* 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, *et al.*, 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, *et al.*, 1983. *Proc Natl Acad Sci USA* 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus *in vitro* (see Cole, *et al.*, 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96).

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to a polymorphic protein (see *e.g.*, U.S. Patent No. 4,946,778). In addition, methodologies can be adapted for the construction of F_{ab} expression libraries (see *e.g.*, Huse, *et al.*, 1989 *Science* 246: 1275-1281) to allow rapid and effective identification of monoclonal F_{ab} fragments with the desired specificity for a polymorphic protein or derivatives, fragments, analogs or homologs thereof. Non-human antibodies can be "humanized" by techniques well known in the art. See *e.g.*, U.S. Patent No. 5,225,539. Antibody fragments that contain the idiotypes to a polymorphic protein may be produced by techniques known in the art including, but not limited to: (i) an $F_{(ab)2}$ fragment produced by pepsin digestion of an antibody molecule; (ii) an F_{ab} fragment generated by reducing the disulfide bridges of an $F_{(ab)2}$ fragment; (iii) an F_{ab} fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv) F_v fragments.

Additionally, recombinant anti-polymorphic protein antibodies, such as chimeric and humanized monoclonal antibodies, comprising both human and non-human portions, which can be made using standard recombinant DNA techniques, are within the scope of the invention. Such chimeric and humanized monoclonal antibodies can be produced by recombinant DNA techniques known in the art, for example using methods described in PCT International Application No. PCT/US86/02269; European Patent Application No. 184,187; European Patent Application No. 171,496; European Patent Application No. 173,494; PCT International Publication No. WO 86/01533; U.S. Pat. No. 4,816,567; European Patent Application No. 125,023; Better *et al.* (1988) *Science* 240:1041-1043; Liu *et al.* (1987) *PNAS* 84:3439-3443; Liu *et al.* (1987) *J Immunol.* 139:3521-3526; Sun *et al.* (1987) *PNAS* 84:214-218; Nishimura *et al.* (1987) *Cancer Res* 47:999-1005; Wood *et al.* (1985) *Nature* 314:446-449; Shaw *et al.* (1988) *J Natl Cancer Inst* 80:1553-1559; Morrison (1985) *Science* 229:1202-1207; Oi *et al.* (1986) *BioTechniques* 4:214; U.S. Pat. No. 5,225,539; Jones *et al.* (1986) *Nature* 321:552-525; Verhoeyan *et al.* (1988) *Science* 239:1534; and Beidler *et al.* (1988) *J Immunol* 141:4053-4060.

In one embodiment, methodologies for the screening of antibodies that possess the desired specificity include, but are not limited to, enzyme-linked immunosorbent assay (ELISA) and other immunologically-mediated techniques known within the art.

Anti-polymorphic protein antibodies may be used in methods known within the art relating to the detection, quantitation and/or cellular or tissue localization of a polymorphic protein (*e.g.*, for use in measuring levels of the polymorphic protein within appropriate physiological samples, for use in diagnostic methods, for use in imaging the protein, and the like). In a given embodiment, antibodies for polymorphic proteins, or derivatives, fragments, analogs or homologs thereof, that contain the antibody-derived CDR, are utilized as pharmacologically-active compounds in therapeutic applications intended to treat a pathology in a subject that arises from the presence of the cSNP allele in the subject.

An anti-polymorphic protein antibody (*e.g.*, monoclonal antibody) can be used to isolate polymorphic proteins by a variety of immunochemical techniques, such as

immunoaffinity chromatography or immunoprecipitation. An anti-polymorphic protein antibody can facilitate the purification of natural polymorphic protein from cells and of recombinantly produced polymorphic proteins expressed in host cells. Moreover, an anti-polymorphic protein antibody can be used to detect polymorphic protein (*e.g.*, in a cellular lysate or cell supernatant) in order to evaluate the abundance and pattern of expression of the polymorphic protein. Anti-polymorphic antibodies can be used diagnostically to monitor protein levels in tissue as part of a clinical testing procedure, *e.g.*, to, for example, determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling (*i.e.*, physically linking) the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, β -galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include ^{125}I , ^{131}I , ^{35}S or ^3H .

EQUIVALENTS

From the foregoing detailed description of the specific embodiments of the invention, it should be apparent that unique compositions and methods of use thereof in SNPs in known genes have been described. Although particular embodiments have been disclosed herein in detail, this has been done by way of example for purposes of illustration only, and is not intended to be limiting with respect to the scope of the appended claims which follow. In particular, it is contemplated by the inventor that various substitutions, alterations, and modifications may be made to the invention without departing from the spirit and scope of the invention as defined by the claims.

Table 1

bioRxiv preprint doi: <https://doi.org/10.1101/2020.03.26.200626>; this version posted March 26, 2020. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

1	2	3	4	5	6	7	8	9	10	11	12	13
Seq ID	CuraGen sequence ID	Base pos. of SNP	Polymorphic sequence	Base before	Base after	Amino acid before	Amino acid after	Type of change	Protein classification of CuraGen gene	Name of protein identified following a BLASTX analysis of the CuraGen sequence	Similarity (pValue) following a BLASTX analysis	Map location
1	cg43921971	1030	GGGTTTGATTG GCGCACCAAGA TC[T/C]CCAACA GCCAGTGTGTG TTTCCCAT	T	C			SILENT- NONCODING	apoptosis	Human Gene Similar to SWISSPROT- ID:P55060 CELLULAR APOPTOSIS SUSCEPTIBILITY PROTEIN - HOMO SAPIENS (HUMAN), 971 aa.	6.10E-68	
3	cg43314087	475	ATGGGTTTTTTT GTTTTGTTTTT GT[Gap]TTTTTTT TTAAAGGCAAG GGGTCT	T	gap			SILENT- NONCODING	ATPase_ associated	Human Gene SWISSPROT- ID:P14415 SODIUM/POTASSIUM- TRANSPORTING ATPASE BETA-2 CHAIN (EC 3.6.1.37) (SODIUM/POTASSIUM-DEPENDENT ATPASE) - HOMO SAPIENS (HUMAN), 290 aa.	4.00E-160	17 (17p)
4	cg43314087	484	TTTGTTTTTGTTT TTGTTTTTTTTT T[Gap]AAAGGCA AAGGGTCTGA AGAGATG	T	gap			SILENT- NONCODING	ATPase_ associated	Human Gene SWISSPROT- ID:P14415 SODIUM/POTASSIUM- TRANSPORTING ATPASE BETA-2 CHAIN (EC 3.6.1.37) (SODIUM/POTASSIUM-DEPENDENT ATPASE) - HOMO SAPIENS (HUMAN), 290 aa.	4.00E-160	17 (17p)
5	cg43132502	200	CATGAGGTGGC ACGAGGCAGGA GTT[G/Gap]GCCA TGCCACCTGGG GGTCACATTG	G	gap			SILENT- NONCODING	ATPase_ associated	Human Gene Similar to SPTREMBL- ID:Q15332 GAMMA SUBUNIT OF SODIUM POTASSIUM ATPASE LIKE - HOMO SAPIENS (HUMAN), 126 aa.	9.40E-58	11
6	cg43988460	4698	ACATAATTTGTA CCAAAAA A[A/Gap]GAAAGG AAAGAAAGGGG TGGCCTGA	A	gap			SILENT- NONCODING	cadherin	Human Gene SWISSPROT- ID:P19022 NEURAL-CADHERIN PRECURSOR (N-CADHERIN) - HOMO SAPIENS (HUMAN), 906 aa.	0.00E+00	18 (18q11.2)

7	cg43988460	4708	TACCAAAAAAAAA AAAGGAAAGGA AA[G/A]AAGGG GTGGCCTGACA CTGGTGCG	G	A			SILENT- NONCODING	cadherin	Human Gene SWISSPROT- ID:P19022 NEURAL-CADHERIN PRECURSOR (N-CADHERIN) - HOMO SAPIENS (HUMAN), 906 aa.	0.00E+00	18 (18q11.2)
8	cg43982945	460	GACACATGTCA GGCTGGGCAG CAG[C/gap]CACT CTGATCAGCAC CAGGTCCCGA	C	gap			SILENT- NONCODING	cathepsin	Human Gene Similar to SWISSPROT- ID:Q26534 CATHEPSIN L PRECURSOR (EC 3.4.22.15) (SMCL1) - SCHISTOSOMA MANSONI (BLOOD FLUKE), 319 aa.	2.00E-80	11
9	cg43266931	96	GGGCGCTAGCG GGGTGCACGG CGG[G/gap]CCG GTAGGCCGCCA GGATCTCGGCG	G	gap			SILENT- NONCODING	chloride channel	Human Gene Similar to SWISSNEW- ID:O15247 CHLORIDE INTRACELLULAR CHANNEL PROTEIN 2 (XAP121) - HOMO SAPIENS (HUMAN), 243 aa.lpcis:SWISSPROT-ID:O15247 CHLORIDE INTRACELLULAR CHANNEL PROTEIN 2 (XAP121) - HOMO SAPIENS (HUMAN), 243 aa.	3.10E-59	9
10	cg43321451	1126	GAAGGCACACA CACACACACAC ACA[C/gap]AGCA AAAGCTAAATCA TCACCCGCG	C	gap			SILENT- NONCODING	collagen	Human Gene SWISSPROT- ID:Q99715 COLLAGEN ALPHA 1(XII) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 3063 aa.lpcis:SPTREMBL-ID:Q99715 COLLAGEN TYPE XII ALPHA-1 PRECURSOR - HOMO SAPIENS (HUMAN), 3063 aa.	0.00E+00	6
11	cg43933757	3195	TCATCTCCCTGC AACCTCCGCCT CCT/CJGGGTTT AAGCGATTCTTG TGCCTCA	T	C			SILENT- NONCODING	complement	Human Gene SWISSPROT- ID:P10643 COMPLEMENT COMPONENT C7 PRECURSOR - HOMO SAPIENS (HUMAN), 843 aa.	0.00E+00	5 (5p13)
12	cg43933757	3212	CCGCCTCCTGG GTTCAAGCGATT CTT/CJGTGCCT CAGCCTCCCAA GCAGCTGG	T	C			SILENT- NONCODING	complement	Human Gene SWISSPROT- ID:P10643 COMPLEMENT COMPONENT C7 PRECURSOR - HOMO SAPIENS (HUMAN), 843 aa.	0.00E+00	5 (5p13)

13	cg43933757	3346	TCCAACTCCTGAG CCTCAGGTAATC C[G/A]CCTGCCT TGGCCTCCCAA AGTGCTG	G	A				SILENT- NONCODING	complem ent	Human Gene SWISSPROT- ID:P10643 COMPLEMENT COMPONENT C7 PRECURSOR - HOMO SAPIENS (HUMAN), 843 aa.	0.00E+00	5 (5p13)
14	cg42185571	2224	CTTAGCTCTACG ATTTAAATCCAT G[T/gap]GTCCAA GGGGGAAAACA TATTATAT	T	gap				SILENT- NONCODING	complem ent	Human Gene SWISSPROT- ID:P02748 COMPLEMENT COMPONENT C9 PRECURSOR - HOMO SAPIENS (HUMAN), 559 aa.	7.70E-308	5 (5p13)
15	cg42185571	2367	TAATATAGATAG TGTCAGTAGCA G[A/gap]ATAGAA TGAACATAAACT ATTAGTT	A	gap				SILENT- NONCODING	complem ent	Human Gene SWISSPROT- ID:P02748 COMPLEMENT COMPONENT C9 PRECURSOR - HOMO SAPIENS (HUMAN), 559 aa.	7.70E-308	5 (5p13)
16	cg43947909	265	GAATTGTCCAGA AGACTTGGCTC AG[C/T]TGGAGG AGCTGATAGAC ATGGCTGT	C	T				SILENT- NONCODING	complem ent	Human Gene Homologous to SWISSPROT-ID:Q07021 COMPLEMENT COMPONENT 1, Q SUBCOMPONENT BINDING PROTEIN PRECURSOR (GLYCOPROTEIN GC1QBP) (GC1Q- R PROTEIN) (HYALURONAN- BINDING PROTEIN 1) (PRE-MRNA SPLICING FACTOR SF2, P32 SUBUNIT) - HOMO SAPIENS (HUMAN), 282 aa.	6.9E-129	17

17	cg43143315	2860	GTGTGTGTGTCT GTGTGTGTGTG TC[C/G]GTGTAT GTGTGTGTGGG TTCTAATG	C	G			SILENT- NONCODING	cyto450	Human Gene SWISSNEW-ID:Q07973 CYTOCHROME P450-CC24 MITOCHONDRIAL PRECURSOR (EC 1.14.-.-) (P450- CC24) (VITAMIN D(3) 24-HYDROXYLASE) (1,25- DIHYDROXYVITAMIN D(3) 24- HYDROXYLASE) (24-OHASE) - HOMO SAPIENS (HUMAN), 513 aa.jpcls:SWISSPROT-ID:Q07973 CYTOCHROME P450-CC24 MITOCHONDRIAL PRECURSOR (EC 1.14.-.-) (P450- CC24) (VITAMIN D(3) 24-HYDROXYLASE) (1,25- DIHYDROXYVITAMIN D(3) 24- HYDROXYLASE) (24-OHASE) - HOMO SAPIENS (HUMAN), 513 aa.	1.9E-279	20
18	cg43327428	1746	AGCAGGCTGGC CTATGTGGTCTA AG[A/G]TTCAGC CTGAAACTCATA GACACTG	A	G			SILENT- NONCODING	cyto450	Human Gene SWISSNEW-ID:P04798 CYTOCHROME P450 1A1 (EC 1.14.14.1) (CYP1A1) (P450-P1) (P450 FORM 6) (P450-C) - HOMO SAPIENS (HUMAN), 512 aa.jpcls:SWISSPROT-ID:P04798 CYTOCHROME P450 1A1 (EC 1.14.14.1) (P450-P1) (P450 FORM 6) (P450-C) (TCDD-INDUCIBLE) - HOMO SAPIENS (HUMAN), 512 aa.	2.5E-279	15 (15q22)
19	cg32296860	376	CAGCACTTTGG GAGGCCGAGGC GGG[T/C]GGATC ACCCGAGGTCA GGAGTTCGA	T	C			SILENT- NONCODING	cytochro me	Human Gene Homologous to SPTREMBL-ID:Q27524 CYTOCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1) - CAENORHABDITIS ELEGANS, 1647 aa (fragment).	6.6E-124	
20	cg32296860	383	TTGGAGGCCG AGCGGGTGGA TCA[C/gap]CCGA GGTCAGGAGTT CGAGACCAGC	C	gap			SILENT- NONCODING	cytochro me	Human Gene Homologous to SPTREMBL-ID:Q27524 CYTOCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1) - CAENORHABDITIS ELEGANS, 1647 aa (fragment).	6.6E-124	

21	cg32296860	385	GGGAGGCCGAG GCGGGTGGATC ACC[C/gap]GAG GTCAGGAGTTC GAGACCAGCCT	C		gap			SILENT- NONCODING	cytochrome	Human Gene Homologous to SPTREMBL-ID:Q27524 CYTOCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1) - CAENORHABDITIS ELEGANS, 1647 aa (fragment).	6.6E-124	
22	cg32296860	397	CGGGTGGATCA CCCGAGGTCAG GAG[T/A]TCGAG ACGAGCCTGGC CAACATGGT	T	A				SILENT- NONCODING	cytochrome	Human Gene Homologous to SPTREMBL-ID:Q27524 CYTOCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1) - CAENORHABDITIS ELEGANS, 1647 aa (fragment).	6.60E-124	
23	cg32296860	439	CAACATGGTGA AACCCTGTCTCT AC[T/C]AAAAATA CAAAAAATTAGCT GGGTGC	T	C				SILENT- NONCODING	cytochrome	Human Gene Homologous to SPTREMBL-ID:Q27524 CYTOCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1) - CAENORHABDITIS ELEGANS, 1647 aa (fragment).	6.60E-124	
24	cg43264442	199	GGGGCGCGGGT GGAGAAGCTGC GGC[A/G]GCGCG GCCCGTAGGAA GGTGCTGTC	A	G				SILENT- NONCODING	dehydrogenase	Human Gene TREMBLNEW- ID:G806944 UDP-GLUCOSE DEHYDROGENASE, UDPGDH=52 KDA SUBUNIT {EC 1.1.1.22} - BOS TAURUS, 468 aa.	8.60E-240	4
25	cg43264442	236	AGGAAGGTGCT GTCCGAACGAT CGG[G/A]ATAGG AGCGGTCCCTG CGCTTGCTG	G	A				SILENT- NONCODING	dehydrogenase	Human Gene TREMBLNEW- ID:G806944 UDP-GLUCOSE DEHYDROGENASE, UDPGDH=52 KDA SUBUNIT {EC 1.1.1.22} - BOS TAURUS, 468 aa.	8.60E-240	4
26	cg43998926	130	GAACCCAAAGAG CCACTGATAACT GG[C/gap]ACAAAT CCAATGAAACA GAGGAAGCA	C	gap				SILENT- NONCODING	dehydrogenase	Human Gene SWISSPROT- ID:P50213 ISOCITRATE DEHYDROGENASE (NAD), MITOCHONDRIAL SUBUNIT ALPHA PRECURSOR (EC 1.1.1.41) (ISOCITRIC DEHYDROGENASE) (NAD+-SPECIFIC ICDH) - HOMO SAPIENS (HUMAN), 366 aa.	1.30E-190	15

27	cg43998926	560	CTCAGGCTGAG TTGCCTCCAGTC TTT[G]GGAATG TCATCTTATACT GGTACTG	T	G				SILENT- NONCODING	dehydrog enase	Human Gene SWISSPROT- ID:P50213 ISOCITRATE DEHYDROGENASE (NAD), MITOCHONDRIAL SUBUNIT ALPHA PRECURSOR (EC 1.1.1.41) (ISOCITRIC DEHYDROGENASE) (NAD+-SPECIFIC ICDH) - HOMO SAPIENS (HUMAN), 366 aa.	1.30E-190	15
28	cg43941594	499	GGTTATAAAAT AGATAACTCGCA G[A/G]GTCATAA ATATCTACAGTT AGTAGA	A	G				SILENT- NONCODING	dehydrog enase	Human Gene Homologous to SWISSPROT-ID:P13707 GLYCEROL- 3-PHOSPHATE DEHYDROGENASE (NAD+), CYTOPLASMIC (EC 1.1.1.8) (GPD-C) (GPDH-C) - MUS MUSCULUS (MOUSE), 348 aa.	1.90E-137	3
29	cg43962927	462	GCCACTCCCTG CTCCCTGCCTG AGC[G/A]CCATT CGCAGTCTTGTT TCCTGTTT	G	A				SILENT- NONCODING	dna_rna _bind	Human Gene SWISSPROT- ID:P38935 DNA-BINDING PROTEIN SMUBP-2 (GLIAL FACTOR-1) (GF-1) HOMO SAPIENS (HUMAN), 993 aa.	0.00E+00	11 (11q13.2)
30	cg43991661	671	CTTGTTTATTAT CTATCATAGACA T[C/G]AAGATGA TCATAGTTAATA CCAATT	C	G				SILENT- NONCODING	dna_rna _bind	Human Gene TREMBLNEW- ID:G2058493 TELOMERIC REPEAT DNA-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 419 aa.	5.10E-224	8
31	cg43991661	737	ACTGTTTAGGC CCAATATTGATA T[A/G]TTAAATGA AGGTATCAGAG AATCTT	A	G				SILENT- NONCODING	dna_rna _bind	Human Gene TREMBLNEW- ID:G2058493 TELOMERIC REPEAT DNA-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 419 aa.	5.10E-224	8
32	cg43310449	206	CTAAAGATTTC TGCTTCAGTGG A[A/G]CTGGCAT ACTGTAATTGCT ATGTGG	A	G				SILENT- NONCODING	dynein	Human Gene SWISSPROT- ID:Q63100 DYNEIN INTERMEDIATE CHAIN 1, CYTOSOLIC (DH IC-1) - RATTUS NORVEGICUS (RAT), 643 aa.	1.0e-312	
33	cg43310449	231	ACTGGCATACT GTAATTGCTATG TG[G/A]AACTTAA TATAACCTCAAC AGCAGC	G	A				SILENT- NONCODING	dynein	Human Gene SWISSPROT- ID:Q63100 DYNEIN INTERMEDIATE CHAIN 1, CYTOSOLIC (DH IC-1) - RATTUS NORVEGICUS (RAT), 643 aa.	1.0e-312	

41	cg43988092	658	TAGCGATACAAA TATATATATATAT [A/gap]TTTATCC AAAAATATGTTT TATACA	A	gap				SILENT- NONCODING	glycoprot ein	Human Gene SWISSPROT- ID:Q01685 TRAM PROTEIN (TRANSLOCATING CHAIN- ASSOCIATING MEMBRANE PROTEIN) - CANIS FAMILIARIS (DOG), 373 aa.	4E-192	8
42	cg43953517	2457	AAGTTCCTGTAG TAGGTAGGGG TA[C/T]TACTAGG GATATCTGTGG CATGATT	C	T				SILENT- NONCODING	glycoprot ein	Human Gene Homologous to SWISSPROT-ID:P51674 MEMBRANE GLYCOPROTEIN M6-A - HOMO SAPIENS (HUMAN), 278 aa.	2.9E-150	4
43	cg43953517	2464	TGTAGTAGGTA GGGGTACTAC TAG[G/C]GATAT CTGTGGCATGA TTATGCATT	G	C				SILENT- NONCODING	glycoprot ein	Human Gene Homologous to SWISSPROT-ID:P51674 MEMBRANE GLYCOPROTEIN M6-A - HOMO SAPIENS (HUMAN), 278 aa.	2.9E-150	4
44	cg43953517	2491	ATATCTGTGGCA TGATTATGCATT C[C/gap]GTAGTA TTATTTAATTAAT TTGGG	C	gap				SILENT- NONCODING	glycoprot ein	Human Gene Homologous to SWISSPROT-ID:P51674 MEMBRANE GLYCOPROTEIN M6-A - HOMO SAPIENS (HUMAN), 278 aa.	2.9E-150	4
45	cg43953517	2517	GTAGTATTATT AATTAATTTGGG G[T/G]TCATTTTG CTTCCTTTCTT TATGC	T	G				SILENT- NONCODING	glycoprot ein	Human Gene Homologous to SWISSPROT-ID:P51674 MEMBRANE GLYCOPROTEIN M6-A - HOMO SAPIENS (HUMAN), 278 aa.	2.9E-150	4
46	cg43953517	2529	AATTAATTTGGG GTTCAATTTGCT T[C/gap]CTTTTC TTTATGCTTAGA TTATCTT	C	gap				SILENT- NONCODING	glycoprot ein	Human Gene Homologous to SWISSPROT-ID:P51674 MEMBRANE GLYCOPROTEIN M6-A - HOMO SAPIENS (HUMAN), 278 aa.	2.9E-150	4
47	cg43953517	2530	ATTAATTTGGGG TTCATTTTGCTT C[C/gap]TTTTCT TTATGCTTAGAT TATCTTA	C	gap				SILENT- NONCODING	glycoprot ein	Human Gene Homologous to SWISSPROT-ID:P51674 MEMBRANE GLYCOPROTEIN M6-A - HOMO SAPIENS (HUMAN), 278 aa.	2.9E-150	4

53	cg43925670	2481	ATGTTCTTGAT TTTTTCCCATC TTTCTACAGACA TAAGTGAGCCT CACTGG	T	C				SILENT- NONCODING	interferon	Human Gene SWISSPROT- ID:Q16666 GAMMA-INTERFERON- INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa. pcis:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment).	0	1
54	cg43925670	2488	TGTATTTTTC CCATCTTTACAG A/C/TATAAGTGA GCCTCACTGGA AATTTT	C	T				SILENT- NONCODING	interferon	Human Gene SWISSPROT- ID:Q16666 GAMMA-INTERFERON- INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa. pcis:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment).	0	1
55	cg43925670	2501	CATCTTTACAGA CATAAGTGAGC CTCTTACTGGA AATTTTTC AAC AGTAGTC	C	T				SILENT- NONCODING	interferon	Human Gene SWISSPROT- ID:Q16666 GAMMA-INTERFERON- INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa. pcis:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment).	0	1

56	cg43925670	2507	TACAGACATAAG TGAGCCTCACT GGAGGAAATTTT TCAACAGTAGTC CAGATC	A	G				SILENT- NONCODING	interferon	Human Gene SWISSPROT- ID:Q16666 GAMMA-INTERFERON- INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa.lpcis:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment)	0	1
57	cg43925670	2513	CATAAGTGAGC CTCACTGGAAAT TTT[C]TTCAACA GTAGTCCAGAT CTTGAGA	T	C				SILENT- NONCODING	interferon	Human Gene SWISSPROT- ID:Q16666 GAMMA-INTERFERON- INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa.lpcis:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment)	0	1
58	cg43925670	2551	CCAGATCTTGA GATCTTCAGAAA TGIC/TAGGAAT CAATGCTTATTT GTGTGAG	C	T				SILENT- NONCODING	interferon	Human Gene SWISSPROT- ID:Q16666 GAMMA-INTERFERON- INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa.lpcis:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment)	0	1

59	cg42489232	2434	ATTTTAGTAGA GACAAGGTTTTG C/C/TATGTTGG CCAGGCTGGTC TCGAACT	C	T		SILENT- NONCODING	interferon	Human Gene SWISSPROT- ID:P48551 INTERFERON- ALPHA/BETA RECEPTOR BETA CHAIN PRECURSOR (IFN-ALPHA- REC) (TYPE I INTERFERON RECEPTOR) (IFN-R) (INTERFERON ALPHA/BETA RECEPTOR- 2) - HOMO SAPIENS (HUMAN), 515 aa.	3.9E-281	21 (21q22.1)
60	cg42489232	2441	GTAGAGACAAG GTTTGGCCATGT TG/G/CJCCAGGC TGGTCTCGAACT CCTGACC	G	C		SILENT- NONCODING	interferon	Human Gene SWISSPROT- ID:P48551 INTERFERON- ALPHA/BETA RECEPTOR BETA CHAIN PRECURSOR (IFN-ALPHA- REC) (TYPE I INTERFERON RECEPTOR) (IFN-R) (INTERFERON ALPHA/BETA RECEPTOR- 2) - HOMO SAPIENS (HUMAN), 515 aa.	3.9E-281	21 (21q22.1)
61	cg42489232	2454	TTTGCCATGTTG GCCAGGCTGGT CT/C/T]GAACTC CTGACCTCAAG CGATCCGC	C	T		SILENT- NONCODING	interferon	Human Gene SWISSPROT- ID:P48551 INTERFERON- ALPHA/BETA RECEPTOR BETA CHAIN PRECURSOR (IFN-ALPHA- REC) (TYPE I INTERFERON RECEPTOR) (IFN-R) (INTERFERON ALPHA/BETA RECEPTOR- 2) - HOMO SAPIENS (HUMAN), 515 aa.	3.9E-281	21 (21q22.1)
62	cg43926168	694	GAAGGGCTCTC CTTCACGGGGA CTG[A/gap]AAAA AAAAAATCATGA AATCCTAAT	A	gap		SILENT- NONCODING	interleukin receptor	Human Gene Similar to SWISSPROT- ID:P18510 INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN PRECURSOR (IL-1RA) (ICIL- 1RA) (IRAP) - HOMO SAPIENS (HUMAN), 177 aa.	8.8E-94	2 (2q14.2)
63	cg43926168	704	CCTTCACGGGG ACTGAAAAA AA[A/gap]TCATG AAATCCTAATTT TCATTTTC	A	gap		SILENT- NONCODING	interleukin receptor	Human Gene Similar to SWISSPROT- ID:P18510 INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN PRECURSOR (IL-1RA) (ICIL- 1RA) (IRAP) - HOMO SAPIENS (HUMAN), 177 aa.	8.8E-94	2 (2q14.2)

64	cg43336163	2889	AGCCGGGAATG CTGCTGCTGCT GCTG/AJCTGCT GCTGCTGCTGC TGGGGGGAT	G	A				SILENT- NONCODING	kinase	Human Gene TREMBLNEW- ID:G300258 MYOTONIC DYSTROPHY KINASE, DM-KINASE {C-TERMINAL, ALTERNATIVELY SPLICED, CLONE DELTA II} - HOMO SAPIENS, 616 aa.	0	19
65	cg43987164	1043	AGGGCAGCCCC TCAGAAGCCCTTC CC[G/A]GCAGAT CCGGGACCCC GTTCTGGT	G	A				SILENT- NONCODING	kinase	Human Gene TREMBLNEW- ID:D1023392 INOSITOL 1,4,5- TRISPHOSPHATE 3-KINASE ISOENZYME (EC 2.7.1.127) - HOMO SAPIENS (HUMAN), 604 aa (fragment).	1.3E-307	
66	cg43119489	2227	TTTTTCATCCTA TCAATTGAATGT G[G/C]CTTGAAA AATCCAGCAAG AGCGGGG	G	C				SILENT- NONCODING	kinase	Human Gene SWISSPROT- ID:Q00537 SERINE/THREONINE- PROTEIN KINASE PCTAIRE-2 (EC 2.7.1.-) - HOMO SAPIENS (HUMAN), 523 aa.	2.7E-282	
67	cg43957170	2164	CTACTAAAAATA CAAAAAATTAGC C[G/A]GGCGTGG TGGCGCATGCC TGTAGTC	G	A				SILENT- NONCODING	kinase	Human Gene SPTREMBL-ID:Q61399 CYCLIN-DEPENDENT PROTEIN KINASE - MUS MUSCULUS (MOUSE), 783 aa.	1.7E-234	
68	cg43957170	2175	ACAAAAAATTAG CCGGCGGTGGT GG[C/T]GCATGC CTGTAGTCCCA GCTACTCG	C	T				SILENT- NONCODING	kinase	Human Gene SPTREMBL-ID:Q61399 CYCLIN-DEPENDENT PROTEIN KINASE - MUS MUSCULUS (MOUSE), 783 aa.	1.70E-234	
69	cg43957170	2179	AAAATTAGCCG GGCGTGGTGGC GCA[T/C]GCCGTG TAGTCCCAGCTA CTCGGGAG	T	C				SILENT- NONCODING	kinase	Human Gene SPTREMBL-ID:Q61399 CYCLIN-DEPENDENT PROTEIN KINASE - MUS MUSCULUS (MOUSE), 783 aa.	1.70E-234	

70	cg38438124	1767	ACTTTGTGTATA TGTGTGTGTGT GT[G/gap]TGTGG GGGGGGGTGA GTGTGTGCG	G	gap			SILENT- NONCODING	kinase	Human Gene SWISSNEW-ID:O70172 PHOSPHATIDYLINOSITOL-4- PHOSPHATE 5-KINASE TYPE II ALPHA (EC 2.7.1.68) (PIP5KII- ALPHA) (1- PHOSPHATIDYLINOSITOL-4- PHOSPHATE KINASE) (PTDINS(4)P- 5-KINASE B ISOFORM) (DIPHOSPHOINOSITIDE KINASE) - MUS MUSCULUS (MOUSE), 405 aa.	2.80E-216	10
71	cg38438124	1769	TTTGTGTATATG TGTGTGTGTGT GT[G/gap]TTGGG GGGGGGGTGAGT GTGTGCGCG	G	gap			SILENT- NONCODING	kinase	Human Gene SWISSNEW-ID:O70172 PHOSPHATIDYLINOSITOL-4- PHOSPHATE 5-KINASE TYPE II ALPHA (EC 2.7.1.68) (PIP5KII- ALPHA) (1- PHOSPHATIDYLINOSITOL-4- PHOSPHATE KINASE) (PTDINS(4)P- 5-KINASE B ISOFORM) (DIPHOSPHOINOSITIDE KINASE) - MUS MUSCULUS (MOUSE), 405 aa.	2.80E-216	10
72	cg42923882	123	AGTGGGCAGGG ACCCCTGGGAGC CTC[C/A]ATTCTC AATGCCCCACC CTTTACCT	C	A			SILENT- NONCODING	kinase	Human Gene SPTREMBL-ID:Q92961 MAP KINASE KINASE MEK5B - HOMO SAPIENS (HUMAN), 448 aa.	1.80E-196	
73	cg43948037	1031	AAAGTTCTCGAA ATGCTTCATCCC C[G/A]ACAAAGC AAATTTTCATGTC CGTCAG	G	A			SILENT- NONCODING	kinase	Human Gene SWISSPROT- ID:Q00532 SERINE/THREONINE- PROTEIN KINASE KIALRE (EC 2.7.1.-) - HOMO SAPIENS (HUMAN), 358 aa.	6.10E-189	
74	cg43948037	1106	CTGTTGCTTTCC CTGGGGTGTC AG[G/A]CTCACC AGGGGAGTCAG AATCTTCT	G	A			SILENT- NONCODING	kinase	Human Gene SWISSPROT- ID:Q00532 SERINE/THREONINE- PROTEIN KINASE KIALRE (EC 2.7.1.-) - HOMO SAPIENS (HUMAN), 358 aa.	6.10E-189	

75	cg43948037	1115	TCCTGGGGTG TCCAGGCTCAC CAG[G/C]GGAGT CAGAACTCTCTG GTTCTCCC	G	C			SILENT- NONCODING	kinase	Human Gene SWISSPROT- ID:Q00532 SERINE/THREONINE- PROTEIN KINASE KIALRE (EC 2.7.1.-) - HOMO SAPIENS (HUMAN), 358 aa.	6.10E-189	
76	cg43948037	1124	TGTCAGGCTC ACCAGGGGAGT CAG[A/G]ATCTT CTGGTTCTCCCT TTTCATCA	A	G			SILENT- NONCODING	kinase	Human Gene SWISSPROT- ID:Q00532 SERINE/THREONINE- PROTEIN KINASE KIALRE (EC 2.7.1.-) - HOMO SAPIENS (HUMAN), 358 aa.	6.10E-189	
77	cg43948037	1134	CACCAGGGGAG TCAGAACTCTCT GGT[C/T]CTCCC TTTTCATCAAGT CTTCTAA	T	C			SILENT- NONCODING	kinase	Human Gene SWISSPROT- ID:Q00532 SERINE/THREONINE- PROTEIN KINASE KIALRE (EC 2.7.1.-) - HOMO SAPIENS (HUMAN), 358 aa.	6.10E-189	
78	cg42703622	2409	TGTGGTTGAC AGATTTTTAAAA TA[G/C]AATTAG AGTATTTGGGT TTTGGT	G	C			SILENT- NONCODING	kinase	Human Gene SPTREMBL-ID:Q12792 PROTEIN TYROSINE KINASE - HOMO SAPIENS (HUMAN), 350 aa.	3.00E-187	12
79	cg43336176	5568	TGCTGCTGCTG CTGCTGCTGGG GGG[G/gap]ATCA CAGACCATTTCT TTCITTCGG	G	gap			SILENT- NONCODING	kinase	Human Gene SPTREMBL-ID:Q16205 MYOTONIN PROTEIN KINASE - HOMO SAPIENS (HUMAN), 625 aa.	1.10E-164	19
80	cg43982923	610	ACGCAGGGGTC CCCGCGGCCGC CGC[G/A]ATGCA GAAATACGAGA AACTGGAAA	G	A			SILENT- NONCODING	kinase	Human Gene SWISSPROT- ID:P49615 CELL DIVISION PROTEIN KINASE 5 (EC 2.7.1.-) (TAU PROTEIN KINASE II CATALYTIC SUBUNIT) (TPKII CATALYTIC SUBUNIT) (KINASE PSSALRE) (CRK6) - MUS MUSCULUS (MOUSE), 292 aa.	3.60E-159	19

85	cg44002977	242	TAGAGGACCAC AGGGTGCAGAG AGG[G/A]TGTCC TGAGGGTCCTT CCTAAGAGG	G	A			SILENT- NONCODING	kinesin	Human Gene Similar to SWISSPROT- ID:Q07866 KINESIN LIGHT CHAIN (KLC) - HOMO SAPIENS (HUMAN), 569 aa.	2.70E-60	6
86	cg27803682	2540	TTGAGCCTCCA GGCTTCTCCTTG AC[G/A]TCATTG CTCTCCTTCCTT GCTGCAA	G	A			SILENT- NONCODING	misc_ch annel	Human Gene Similar to SPTREMBL- ID:P91197 SIMILAR TO LIGAND- GATED IONIC CHANNEL PROTEIN - CAENORHABDITIS ELEGANS, 461 aa.	3.50E-81	
87	cg43971768	2349	GAACTGCAGTC ATGCACAGCTG GCG[A/G]CCAGC CAAAGGCATTTT ACTGAGCA	A	G			SILENT- NONCODING	nucl_rec pt	Human Gene SWISSNEW-ID:Q61324 ARYL HYDROCARBON RECEPTOR NUCLEAR TRANSLOCATOR 2 (ARNT PROTEIN 2) - MUS MUSCULUS (MOUSE), 712 aa.	0.00E+00	15
88	cg43987181	1358	AAGCTTAGTACT AAAAAGTCAAAA TTT[A]TTTTGCA TGATAGAGGAG TGTAAG	T	A			SILENT- NONCODING	nucl_rec pt	Human Gene SWISSNEW-ID:Q13451 51 KD FK506-BINDING PROTEIN (FKBP51) (PEPTIDYL-PROLYL CIS- TRANS ISOMERASE) (EC 5.2.1.8) (PPIASE) (ROTAMASE) (54 KD PROGESTERONE RECEPTOR- ASSOCIATED IMMUNOPHILIN) (FKBP54) (P54) (FF1 ANTIGEN) - HOMO SAPIENS (HUMAN), 457 aa. Jpcls:SWISSPROT-ID:Q13451 51 KD FK506-BINDING PROTEIN (FKBP51) (PEPTIDYL-PROLYL CIS- TRANS ISOMERASE) (EC 5.2.1.8) (PPIASE) (ROTAMASE) (54 KD PROGESTERONE RECEPTOR- ASSOCIATED IMMUNOPHILIN) (FKBP54) (P54) (FF1 ANTIGEN) - HOMO SAPIENS (HUMAN), 457 aa.	9.40E-248	6

89	cg43263644	143	GCCGGGACAGT GTTGTACAGTGT TTT/CJGGGCAT GCACGTGATAC TCACACAG	T	C			SILENT- NONCODING	nuc _l _rec pt	Human Gene SWISSPROT- ID:Q03181 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR BETA (PPAR-BETA) (PPAR-DELTA) (NUCLEAR HORMONE RECEPTOR 1) (NUC1) (NUC1) - HOMO SAPIENS (HUMAN), 441 aa.	4.70E-237	6
90	cg44131079	3497	CGGTGATATTAC AAAACAATGAAT TTC/TJGGAACAT TATAGATTGGC ACCTC	C	T			SILENT- NONCODING	nuclease	Human Gene SWISSNEW-ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] - HOMO SAPIENS (HUMAN), 874 aa.lpcis:SWISSPROT-ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) - HOMO SAPIENS (HUMAN), 874 aa.	0.00E+00	
91	cg44031914	153	GCACAGGGGAG TGAGGGCAGGG CGC/T/CJCGCAG GGGGCACGCAG GGAGGGCCCC	T	C			SILENT- NONCODING	oncogen e	Human Gene SWISSPROT- ID:Q01543 FLI-1 ONCOGENE (ERGB TRANSCRIPTION FACTOR) - HOMO SAPIENS (HUMAN), 452 aa.	4.70E-253 (11q24)	11
92	cg43932550	3136	CATCATAGAACT CCTGTGGATCT C[G/A]TAGAGCT CAGGCACITTTG AAGAAGA	G	A			SILENT- NONCODING	oncogen e	Human Gene SPTREMBL-ID:Q13746 BCR-ABL MRNA OF ACUTE LYMPHOCTIC LEUKAEMIA (ALL) PATIENTS - HOMO SAPIENS (HUMAN), 386 aa.	2.30E-205 (22q11.2 1)	22
93	cg43932550	3312	GACAGGACCCA TTTTCTCATCTC CAI/GJGCCCTT TTCCAAGTCCAG CTCACTC	A	G			SILENT- NONCODING	oncogen e	Human Gene SPTREMBL-ID:Q13746 BCR-ABL MRNA OF ACUTE LYMPHOCTIC LEUKAEMIA (ALL) PATIENTS - HOMO SAPIENS (HUMAN), 386 aa.	2.30E-205 (22q11.2 1)	22

94	cg43967268	598	ACGAGAGAAAGG AGCAGCTGAAA GTG[A]CCTGG ACTCCAGCCCT GGCTGTTGT	G	A				SILENT- NONCODING	oncogene	Human Gene Similar to SWISSPROT- ID:P24407 RAS-RELATED PROTEIN RAB-8 (ONCOGENE C-MEL) - HOMO SAPIENS (HUMAN), AND CANIS FAMILIARIS (DOG), 207 aa.	1.90E-52	
95	cg43920534	1076	CGTCACTATGTA CTTGGTTTTCGG CT[Gap]TTTTTT CCTTAAAAA AAGGCC	T	gap				SILENT- NONCODING	phosphatase	Human Gene SPTREMBL-ID:Q10728 SERINE/THREONINE PROTEIN PHOSPHATASE PP1 SMOOTH MUSCLE REGULATORY M110 SUBUNIT (110 KDA SUBUNIT) - RATTUS NORVEGICUS (RAT), 976 aa.	0.00E+00	12
96	cg43920534	763	CTTCATAAAACC AATCGAGAGAG AG[A]gap]GGACT TAAATCCTGCT TACCAAAA	A	gap				SILENT- NONCODING	phosphatase	Human Gene SPTREMBL-ID:Q10728 SERINE/THREONINE PROTEIN PHOSPHATASE PP1 SMOOTH MUSCLE REGULATORY M110 SUBUNIT (110 KDA SUBUNIT) - RATTUS NORVEGICUS (RAT), 976 aa.	0.00E+00	12
97	cg43926887	1786	ATTGTTTTCAAC ATGAAGTAAAGA A[T]A]AACGTTGA GGCCTTTACTAT TAGCT	T	A				SILENT- NONCODING	phosphatase	Human Gene SWISSPROT- ID:Q06190 PROTEIN PHOSPHATASE PP2A, 130 KD REGULATORY SUBUNIT (PR130) - HOMO SAPIENS (HUMAN), 1150 aa.	0.00E+00	3
98	cg43926887	1838	GTCTAATACTCC TGGAGGAAGG AA[T]A]ATATCTA TCTAGTAAGAAT TTTAAT	T	A				SILENT- NONCODING	phosphatase	Human Gene SWISSPROT- ID:Q06190 PROTEIN PHOSPHATASE PP2A, 130 KD REGULATORY SUBUNIT (PR130) - HOMO SAPIENS (HUMAN), 1150 aa.	0.00E+00	3
99	cg43088901	2303	GAGCACCGTGT CAAGCTGCTCT GAG[C]C]CACAG TGGGATGAACC AGCCGGGGC	C	T				SILENT- NONCODING	phosphatase	Human Gene SWISSNEW-ID:P30304 M-PHASE INDUCER PHOSPHATASE 1 (EC 3.1.3.48) - HOMO SAPIENS (HUMAN), 523 aa. pcds:SWISSPROT-ID:P30304 M- PHASE INDUCER PHOSPHATASE 1 (EC 3.1.3.48) - HOMO SAPIENS (HUMAN), 523 aa.	4.00E-288	3 (3p21)

100	cg43920213	3664	GTGAGCCATAAT ATGATGGCCAG CA[G/gap]GTGG CGCTGCCTTCC ACCCATGGTG	G	gap			SILENT- NONCODING	phosphatase	Human Gene Similar to SWISSPROT- ID:P51452 DUAL SPECIFICITY PROTEIN PHOSPHATASE 3 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE VHR) - HOMO SAPIENS (HUMAN), 185 aa.	6.00E-81	17
101	cg43969348	648	TGGGGGAATG GGCCTCTTGGG GGT[C/gap]TCAC TGCACGGCTTG TTCATTGGCA	C	gap			SILENT- NONCODING	polymerase	Human Gene Similar to SPTREMBL- ID:Q15370 RNA POLYMERASE II TRANSCRIPTION FACTOR SIII P18 SUBUNIT - HOMO SAPIENS (HUMAN), 118 aa.	3.90E-59	16
102	cg43966692	331	TACGAATTGGCA TATTTGTTATTT [C/gap]TCAGTTT GTGAAATGTCC TTAATT	C	gap			SILENT- NONCODING	polymerase	Human Gene Similar to SPTREMBL- ID:Q15369 RNA POLYMERASE II ELONGATION FACTOR SIII, P15 SUBUNIT - HOMO SAPIENS (HUMAN), 112 aa.	4.00E-57	8
103	cg43265754	4375	CGAGACCAGCC TGGCCAACATG GTG[A/C]AACCC CATCTCTACTAA AAATACAA	A	C			SILENT- NONCODING	potassium channel	Human Gene SWISSPROT- ID:P48544 G PROTEIN-ACTIVATED INWARD RECTIFIER POTASSIUM CHANNEL 4 (GIRK4) (POTASSIUM CHANNEL, INWARDLY RECTIFYING, SUBFAMILY J, MEMBER 5) (HEART KATP CHANNEL) (KATP-1) (CARDIAC INWARD RECTIFIER) (CIR) (KIR3.4) - HOMO SAPIENS (HUMAN), 419 aa.	6.70E-185	
104	cg43265754	4389	CCAAATGGTG AAACCCCATCTC TA[C/T]TAAAAAT ACAAAAATTAGC CGGGCG	C	T			SILENT- NONCODING	potassium channel	Human Gene SWISSPROT- ID:P48544 G PROTEIN-ACTIVATED INWARD RECTIFIER POTASSIUM CHANNEL 4 (GIRK4) (POTASSIUM CHANNEL, INWARDLY RECTIFYING, SUBFAMILY J, MEMBER 5) (HEART KATP CHANNEL) (KATP-1) (CARDIAC INWARD RECTIFIER) (CIR) (KIR3.4) - HOMO SAPIENS (HUMAN), 419 aa.	6.70E-185	

105	cg43922227	538	ATGTTGTGTTGG GTCCCCAGATT CCCTTATTTGAT TTTCTTGCATCA TTTTCT	C	T			SILENT- NONCODING	reductase	Human Gene Homologous to SWISSPROT-ID:P36959 GMP REDUCTASE (EC 1.6.6.8) (GUANOSINE 5'-MONOPHOSPHATE OXIDOREDUCTASE) - HOMO SAPIENS (HUMAN), 345 aa.	7.70E-150	14
106	cg43927549	1020	GTAAGCAGCAC ACTAGGAGGCC CAG[G]gap]CGC AGGCAAAAGAGA AGATGGTGCTG	G	gap			SILENT- NONCODING	reductase	Human Gene Homologous to SWISSPROT-ID:P16083 NAD(P)H DEHYDROGENASE (QUINONE) 2 (EC 1.6.99.2) (QUINONE REDUCTASE) (DT-DIAPHORASE) (AZOREDUCTASE) (PHYLLOQUINONE REDUCTASE) (MENADIONE REDUCTASE) - HOMO SAPIENS (HUMAN), 231 aa.	1.60E-124	6 (6pter)
107	cg43957486	4041	TGTATCATAGAA ATGTAACTTTTG T[A]GJAGACAAA GGTTTTCTCTT CTATTT	A	G			SILENT- NONCODING	struct	Human Gene SWISSPROT- ID:P07204 THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM) (CD141 ANTIGEN) - HOMO SAPIENS (HUMAN), 575 aa.	0.00E+00	20 (20p11.2)
108	cg43973080	779	GACACTAGGAA TTTCTTAAAAAG AA[A]gap]GATGT TGGAAAGCAGAA CACTTACTA	A	gap			SILENT- NONCODING	struct	Human Gene TREMBLNEW- ID:G2304981 MYOSIN VI - HOMO SAPIENS (HUMAN), 1262 aa.	0.00E+00	6
109	cg42914441	2306	CTCTGACCTGA GTCTTTGTTTTA AG[A]GJAGTATTT GTCTTCCTTTGT CTAATG	A	G			SILENT- NONCODING	struct	Human Gene Homologous to SWISSPROT-ID:P26044 RADIXIN (MOESIN B) - SUS SCROFA (PIG), 583 aa.	5.40E-133	22 (22q12.2)
110	cg43942318	1006	GGACACCCCTCG GACCCCTCGAAA ACG[C/T]CTCAG GAGCTATGAAG ACATGATTG	C	T			SILENT- NONCODING	struct	Human Gene Homologous to SPTREMBL-ID:O00379 DELTA- CATENIN - HOMO SAPIENS (HUMAN), 792 aa.	4.80E-123	11

111	cg43929933	431	CAGGCCAGGCC TGTGTGTCCAC CTG[C/G]ACAGG CATTCTCCTTGT TCCAGAAA	C	G				SILENT- NONCODING	struct	Human Gene Homologous to SPTREMBL-ID:P97756 CA2+/CALMODULIN-DEPENDENT PROTEIN KINASE IV KINASE ISOFORM - RATTUS NORVEGICUS (RAT), 505 aa.	1.80E-117	12
112	cg43929933	541	CGCAGCCCCAA GTGTCAACAAG GGG[C/T]TCAAT AAGGCTTTCTG GGAGCCACT	C	T				SILENT- NONCODING	struct	Human Gene Homologous to SPTREMBL-ID:P97756 CA2+/CALMODULIN-DEPENDENT PROTEIN KINASE IV KINASE ISOFORM - RATTUS NORVEGICUS (RAT), 505 aa.	1.80E-117	12
113	cg43929933	590	CTGGCAGCTGG TGGGATGGAAG GGG[G/gap]AGG TGGAAAAGGGC AGAGGAAATGG	G	gap				SILENT- NONCODING	struct	Human Gene Homologous to SPTREMBL-ID:P97756 CA2+/CALMODULIN-DEPENDENT PROTEIN KINASE IV KINASE ISOFORM - RATTUS NORVEGICUS (RAT), 505 aa.	1.80E-117	12
114	cg43070037	7268	AGGTCAGGAGT TTGAGACCAGC CTA[G/A]CCAAC ATGGTGAAACC CCATCTCTA	G	A				SILENT- NONCODING	synthase	Human Gene SWISSPROT- ID:P35421 PHOSPHORIBOSYLFORMYLGLYCI NAMIDINE SYNTHASE (EC 6.3.5.3) (FGAM SYNTHASE) (FORMYLGLYCINAMIDE RIBOTIDE AMIDOTRANSFERASE) (FGARAT) (ADENOSINE-2) (FGAMS) (FORMYLGLYCINAMIDE RIBOTIDE SYNTHETASE) - DROSOPHILA MELANOGASTER (FRUIT FLY), 1354 aa.	0.00E+00	

115	cg43070037	7269	GGTCAGGAGTT TGAGACCAGCC TAG[C/G]CAACA TGGTGAAACCC CATCTCTAC	C	G				SILENT- NONCODING	synthase	Human Gene SWISSPROT- ID:P35421 PHOSPHORIBOSYLFORMYLGLYCINAMINE SYNTHASE (EC 6.3.5.3) (FGAM SYNTHASE) (FORMYLGLYCINAMIDE RIBOTIDE AMIDOTRANSFERASE) (FGARAT) (ADENOSINE-2) (FGAMS) (FORMYLGLYCINAMIDE RIBOTIDE SYNTHETASE) - DROSOPHILA MELANOGASTER (FRUIT FLY), 1354 aa.	0.00E+00	
116	cg43070037	7352	GTGGGTGCCTG TAATCCCAGCTA CT[C/T]GGGAGG CTGAGGCAGGA GAATCACC	C	T				SILENT- NONCODING	synthase	Human Gene SWISSPROT- ID:P35421 PHOSPHORIBOSYLFORMYLGLYCINAMINE SYNTHASE (EC 6.3.5.3) (FGAM SYNTHASE) (FORMYLGLYCINAMIDE RIBOTIDE AMIDOTRANSFERASE) (FGARAT) (ADENOSINE-2) (FGAMS) (FORMYLGLYCINAMIDE RIBOTIDE SYNTHETASE) - DROSOPHILA MELANOGASTER (FRUIT FLY), 1354 aa.	0.00E+00	
117	cg43070037	7365	ATCCAGCTACT CGGGAGGCTGA GG[C/T]AGGAGA ATCACCTGAACC TAGGAGG	C	T				SILENT- NONCODING	synthase	Human Gene SWISSPROT- ID:P35421 PHOSPHORIBOSYLFORMYLGLYCINAMINE SYNTHASE (EC 6.3.5.3) (FGAM SYNTHASE) (FORMYLGLYCINAMIDE RIBOTIDE AMIDOTRANSFERASE) (FGARAT) (ADENOSINE-2) (FGAMS) (FORMYLGLYCINAMIDE RIBOTIDE SYNTHETASE) - DROSOPHILA MELANOGASTER (FRUIT FLY), 1354 aa.	0.00E+00	

118	cg43070037	7366	TCCCAGCTACTCA GGGAGGCTGAG GC[A/G]GGAGAA TCACCTGAACCT AGGAGGC	A	G				SILENT- NONCODING	synthase	Human Gene SWISSPROT- ID:P35421 PHOSPHORIBOSYLFORMYLGLYCI NAMIDINE SYNTHASE (EC 6.3.5.3) (FGAM SYNTHASE) (FORMYLGLYCINAMIDE RIBOTIDE AMIDOTRANSFERASE) (FGARAT) (ADENOSINE-2) (FGAMS) (FORMYLGLYCINAMIDE RIBOTIDE SYNTHETASE) - DROSOPHILA MELANOGASTER (FRUIT FLY), 1354 aa.	0.00E+00	
119	cg43123664	240	AGTACGCCAGC CCGGGGCGGCC CCG[A/C]ATGTA CATGTTCCACG CGGGATTCC	A	C				SILENT- NONCODING	synthase	Human Gene Similar to SWISSPROT- ID:O35696 ALPHA-2,8- SIALYLTRANSFERASE (EC 2.4.99.-) (ST8SIAII) (SIALYLTRANSFERASE X) (STX) (POLYSIALIC ACID SYNTHASE) - MUS MUSCULUS (MOUSE), 375 aa.	3.10E-59	18
120	cg21428405	17	NACGCGTTGGC GTCGTT[C]CTC GTTGAGCTCATC AATCCACCAC	T	C				SILENT- NONCODING	synthase	Human Gene Similar to SWISSNEW- ID:P54876 PHOSPHORIBOSYLFORMYLGLYCI NAMIDINE SYNTHASE II (EC 6.3.5.3) (FGAM SYNTHASE II) - MYCOBACTERIUM TUBERCULOSIS, 754 aa.	2.20E-56	
121	cg43982633	811	ACACAGCCCCA GTTTGCTTTACA GC[C/G]CAAGTT ACAAACTGTCCC TTTAAAA	C	G				SILENT- NONCODING	tgfrecept or	Human Gene SWISSPROT- ID:P56159 GDNF RECEPTOR ALPHA PRECURSOR (GDNFR- ALPHA) (TGF-BETA RELATED NEUROTROPHIC FACTOR RECEPTOR 1) - HOMO SAPIENS (HUMAN), 464 aa.	1.50E-254	
122	cg43054268	312	TCTAGATATTTA ACTGACCCACTA T[A/gap]TTCCTC AAGGATACTGC ATTGGAC	A	gap				SILENT- NONCODING	thioester ase	Human Gene Similar to TREMBLNEW-ID:E307161 MITOCHONDRIAL VERY-LONG- CHAIN ACYL-COA THIOESTERASE - RATTUS NORVEGICUS (RAT), 453 aa.	3.50E-83	9

123	cg43054268	448	GACTATATGATC AAAGCCTTATAG C[A/gap]AAAAAA ATTTTAAATATT TGCAAA	A	gap				SILENT- NONCODING	thioester ase	Human Gene Similar to TREMBLNEW-ID:E307161 MITOCHONDRIAL VERY-LONG- CHAIN ACYL-COA THIOESTERASE - RATTUS NORVEGICUS (RAT), 453 aa.	3.50E-83	9
124	cg43943775	259	TGAAGATTACCC CCACACCTGTG TG[A/G]CAAGTG ATCAAAAAGGAA CAGGACC	A	G				SILENT- NONCODING	tm7	Human Gene SWISSPROT- ID:P21554 CANNABINOID RECEPTOR 1 (CB1) (CB-R) (CANN6) - HOMO SAPIENS (HUMAN), 472 aa.	5.40E-252	6 (6q14)
125	cg42886565	3473	GGCAACAAAAG CGAACTCCATC TC[A/gap]AAAAA AAAGAGCTATAG GATCTTTA	A	gap				SILENT- NONCODING	tm7	Human Gene SWISSPROT- ID:P25116 THROMBIN RECEPTOR PRECURSOR - HOMO SAPIENS (HUMAN), 425 aa.	4.40E-225	5 (5q13)
126	cg42886565	3481	AAGCGAAACTC CATCTCAAAAA AA[A/gap]GAGCT ATAGGATCTTTA CAATATAT	A	gap				SILENT- NONCODING	tm7	Human Gene SWISSPROT- ID:P25116 THROMBIN RECEPTOR PRECURSOR - HOMO SAPIENS (HUMAN), 425 aa.	4.40E-225	5 (5q13)
127	cg42886565	4462	TCCTCTGTCTGC TGGCTGGCCGC GT[G/A]TATGAA GAAGACTAATTG GACACAG	G	A				SILENT- NONCODING	tm7	Human Gene SWISSPROT- ID:P25116 THROMBIN RECEPTOR PRECURSOR - HOMO SAPIENS (HUMAN), 425 aa.	4.40E-225	5 (5q13)
128	cg42886565	4483	GCGTGTATGAA GAAGACTAATTG GA[C/T]ACAGAG CCGTGATGAATT AAAGTCT	C	T				SILENT- NONCODING	tm7	Human Gene SWISSPROT- ID:P25116 THROMBIN RECEPTOR PRECURSOR - HOMO SAPIENS (HUMAN), 425 aa.	4.40E-225	5 (5q13)
129	cg43307001	1796	GCCTCCCGGGT TCAAGTGATTCT CC[T/C]GCCTCA GCCTCCCCAGTA GCTGGGAT	T	C				SILENT- NONCODING	tm7	Human Gene SWISSPROT- ID:P35348 ALPHA-1A ADRENERGIC RECEPTOR (ALPHA 1A- ADRENOCEPTOR) (ALPHA-1C ADRENERGIC RECEPTOR) - HOMO SAPIENS (HUMAN), 466 aa.	2.50E-199	

130	cg43307001	1898	GGGGTTTCACC ATGTTGGCCAG GCT[G/A]GTCTC GAACCTCCTGAC CTCAAGTGA	G	A			SILENT- NONCODING	tm7	Human Gene SWISSPROT- ID:P35348 ALPHA-1A ADRENERGIC RECEPTOR (ALPHA 1A- ADRENOCEPTOR) (ALPHA-1C ADRENERGIC RECEPTOR) - HOMO SAPIENS (HUMAN), 466 aa.	2.50E-199	
131	cg43307001	1909	ATGTTGGCCAG GCTGGTCTCGA ACT[C/T]CTGAC CTCAAGTGATCC GCCACCT	C	T			SILENT- NONCODING	tm7	Human Gene SWISSPROT- ID:P35348 ALPHA-1A ADRENERGIC RECEPTOR (ALPHA 1A- ADRENOCEPTOR) (ALPHA-1C ADRENERGIC RECEPTOR) - HOMO SAPIENS (HUMAN), 466 aa.	2.50E-199	
132	cg43047341	2113	GGTGGATCACC TGAGGTCACGA GTT[C/T]GAGAC CAGCCTGACCA ACATGGAGA	C	T			SILENT- NONCODING	tm7	Human Gene SWISSPROT- ID:P21731 THROMBOXANE A2 RECEPTOR (TXA2-R) (PROSTANOID TP RECEPTOR) - HOMO SAPIENS (HUMAN), 369 aa.	2.80E-190	
133	cg43965652	891	TCCATTTCTTTT TCTTTTTTTTTT [T/gap]TAAGTGA GACTACATTGG CAAATGG	T	gap			SILENT- NONCODING	tnf	Human Gene Homologous to SPTREMBL-ID:Q99732 TNF-ALPHA INDUCIBLE RESPONSIVE ELEMENT - HOMO SAPIENS (HUMAN), 228 aa.	4.50E-121	16
134	cg43965652	892	CCATTTCTTTT CTTTTTTTTTTT [T/gap]AAGTGAG ACTACATTGGCA AATGGG	T	gap			SILENT- NONCODING	tnf	Human Gene Homologous to SPTREMBL-ID:Q99732 TNF-ALPHA INDUCIBLE RESPONSIVE ELEMENT - HOMO SAPIENS (HUMAN), 228 aa.	4.50E-121	16
135	cg43965652	412	TTCCAAACATCA AATGAAGGGGG AT[C/gap]AATGG TTACCACTATCG TTTTCAAC	C	gap			SILENT- NONCODING	tnf	Human Gene Homologous to SPTREMBL-ID:Q99732 TNF-ALPHA INDUCIBLE RESPONSIVE ELEMENT - HOMO SAPIENS (HUMAN), 228 aa.	4.50E-121	16
136	cg43985709	933	AGCTCACTTTGG CCCTCTCCACC C[A/G]TCCCAAC CCCATTGCTAAC AACATG	A	G			SILENT- NONCODING	tnf	Human Gene Similar to SWISSPROT- ID:Q13829 TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN) - HOMO SAPIENS (HUMAN), 316 aa.	1.70E-51	16

137	cg44027791	1118	GCCACAGGGCT CCTTTCCACCAG GG[G/gap]CCCA GGAGGACACA GGTGGGGGAC	G	gap				SILENT- NONCODING	transcript factor	Human Gene SWISSPROT- ID:Q02086 TRANSCRIPTION FACTOR SP2 (KIAA0048) - HOMO SAPIENS (HUMAN), 606 aa.	0.00E+00	17
138	cg44027791	1173	TCCTCAGGGCC TCCCGCCGCAG TTG[G/A]CCTTA CAAGTCTTCGT GACCCAGGT	G	A				SILENT- NONCODING	transcript factor	Human Gene SWISSPROT- ID:Q02086 TRANSCRIPTION FACTOR SP2 (KIAA0048) - HOMO SAPIENS (HUMAN), 606 aa.	0.00E+00	17
139	cg44027791	916	AAGGTTCCCA CGCGTCCTGGT TTA[G/A]AACGT CTCATTGGGCA CGGCCAGTG	G	A				SILENT- NONCODING	transcript factor	Human Gene SWISSPROT- ID:Q02086 TRANSCRIPTION FACTOR SP2 (KIAA0048) - HOMO SAPIENS (HUMAN), 606 aa.	0.00E+00	17
140	cg44027791	930	GTCTGGTTTAG AACGTCTCATTG G[G/gap]CACGG CCAGTGTCCAC AGTCTGGGC	G	gap				SILENT- NONCODING	transcript factor	Human Gene SWISSPROT- ID:Q02086 TRANSCRIPTION FACTOR SP2 (KIAA0048) - HOMO SAPIENS (HUMAN), 606 aa.	0.00E+00	17
141	cg43984418	923	TATGCAATGTTT AGCAATTTTTTT TTT[gap]TCACAG CACTAGAGACC CTGTTAAA	T	gap				SILENT- NONCODING	transcript factor	Human Gene SWISSPROT- ID:P23771 TRANS-ACTING T-CELL SPECIFIC TRANSCRIPTION FACTOR GATA-3 - HOMO SAPIENS (HUMAN), 443 aa.	2.40E-255 (10p15)	10
142	cg43984418	937	CATTTTTTTTTT CACAGCACTAG A[G/A]ACCCCTGT TAAATAGGGGAT ATGAGT	G	A				SILENT- NONCODING	transcript factor	Human Gene SWISSPROT- ID:P23771 TRANS-ACTING T-CELL SPECIFIC TRANSCRIPTION FACTOR GATA-3 - HOMO SAPIENS (HUMAN), 443 aa.	2.40E-255 (10p15)	10
143	cg43945210	543	CAGACAGACAC AAGGTTCTTTTT TTT[gap]GTTTG TTTTGTTTTTCC TCGCCAAC	T	gap				SILENT- NONCODING	transcript factor	Human Gene SWISSPROT- ID:Q60632 COUP TRANSCRIPTION FACTOR 1 (COUP-TF1) (COUP-TFI) - MUS MUSCULUS (MOUSE), 422 aa.	6.40E-235	5

144	cg43917396	915	TAGGGGCTGAA ACGCAGTCGGG GCC[G/gap]GGC ACTGCCACAGGA AGGACTCCGG	G	gap				SILENT- NONCODING	transcript factor	Human Gene Similar to TREMBLNEW-ID:G2920821 TRANSCRIPTION FACTOR T-BOX 5 HOMO SAPIENS (HUMAN), 518 aa.	6.90E-68	
145	cg43949162	510	TAGACAATACCA TCTCTAGGAACA C[A/G]CTGTGCAC TCACACATGGAT GTGTTG	A	G				SILENT- NONCODING	transfere se	Human Gene Homologous to TREMBLNEW-ID:G2738933 GLUTATHIONE TRANSFERASE (EC 2.5.1.18) - HOMO SAPIENS (HUMAN), 222 aa.	1.30E-115	6
146	cg41653463	2407	TGTGCGTGCGT GTGTGTGTGTG TGT[G/gap]TGTA TCGTGTGTGTGT GTTTGTTT	G	gap				SILENT- NONCODING	transport	Human Gene SWISSPROT- ID:P31641 SODIUM- AND CHLORIDE-DEPENDENT TAURINE TRANSPORTER - HOMO SAPIENS (HUMAN), 620 aa.	0.00E+00	3 (3p25)
147	cg41653463	2408	GTGCGTGCGTG TGTGTGTGTGT GTG[T/gap]GTAT CGTGTGTGTGT GTTTGTTT	T	gap				SILENT- NONCODING	transport	Human Gene SWISSPROT- ID:P31641 SODIUM- AND CHLORIDE-DEPENDENT TAURINE TRANSPORTER - HOMO SAPIENS (HUMAN), 620 aa.	0.00E+00	3 (3p25)
148	cg43285429	388	CCCAGTCAAGA TAAGGAGGATC CCA[G/A]CAGCT CCCCCTCCGAGG TTGGGCTCT	G	A				SILENT- NONCODING	transport	Human Gene SWISSNEW-ID:P02730 BAND 3 ANION TRANSPORT PROTEIN (ANION EXCHANGE PROTEIN 1) (AE 1) - HOMO SAPIENS (HUMAN), 911 aa.lpcis:SWISSPROT-ID:P02730 BAND 3 ANION TRANSPORT PROTEIN (ANION EXCHANGE PROTEIN 1) (AE 1) - HOMO SAPIENS (HUMAN), 911 aa.	0.00E+00	17 (17q21)
149	cg43918636	3322	AGCAGCAGCTG TTGGAGTAGAA CCG[C/A]GTCCA GGCGCGGACCA TCCTCATCG	C	A				SILENT- NONCODING	transport	Human Gene Similar to SWISSPROT- ID:Q15012 GOLGI 4- TRANSMEMBRANE SPANNING TRANSPORTER MTP (KIAA0108) - HOMO SAPIENS (HUMAN), 233 aa.	5.40E-52	

157	cg43936083	189	GCTAACTGGT ACAGTTATAAAA AC[A/G]CAAAA GGAGCCTGGGA AACAGCAA	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O15089 KIAA0385 - HOMO SAPIENS (HUMAN), 1370 aa.	0.00E+00	
158	cg43936393	382	AAAAACAAGTTT CAGTAAAAAAA A[A/gap]ACTAAA ACAAACACTGAA GTAGAGT	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD22032 THYROID HORMONE RECEPTOR- ASSOCIATED PROTEIN COMPLEX COMPONENT TRAP240 - HOMO SAPIENS (HUMAN), 2174 aa.	0.00E+00	17
159	cg43936393	383	AAAAACAAGTTTC AGTAAAAAAA A[A/gap]CTAAA CAAACTACTGAA GTAGAGTT	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD22032 THYROID HORMONE RECEPTOR- ASSOCIATED PROTEIN COMPLEX COMPONENT TRAP240 - HOMO SAPIENS (HUMAN), 2174 aa.	0.00E+00	17
160	cg43940465	304	ACTGTATTATTT ATTACATGGGC T[G/A]AAAGCAA AGAAAAATGAGT CCCTTC	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O60300 KIAA0553 PROTEIN - HOMO SAPIENS (HUMAN), 1095 aa (fragment).	0.00E+00	
161	cg43940880	10186	TAGTTTGTAAAG ACTGTACAAAA A[A/gap]TGCTTC TGGAGATTCTT TGGCAGA	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:P53794 SODIUM/MYO- INOSITOL COTRANSPORTER (NA(+)/MYO-INOSITOL COTRANSPORTER) - Homo sapiens (Human), 718 aa.	0.00E+00	21
162	cg43950657	1956	TTTGGGATCCTG ATCAATTCCTTC T[G/A]ATGTTGT GAAATGACAAA GTTGG	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW- ACC:Q13009 T-LYMPHOMA INVASION AND METASTASIS INDUCING PROTEIN 1 (TIAM1 PROTEIN) - Homo sapiens (Human), 1591 aa.	0.00E+00 (21q22.1)	21

163	cg43950657	2033	CAGCTGCCAAA ACCGTGTGTGC AAG[A/G]GCGCG ACCTAAGGGGA CATTCTTGT	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW- ACC:Q13009 T-LYMPHOMA INVASION AND METASTASIS INDUCING PROTEIN 1 (TIAM1 PROTEIN) - Homo sapiens (Human), 1591 aa.	0.00E+00	21 (21q22.1)
164	cg43973740	485	TGAAGCAACAA ACAAACAAAAA A[A/gap]GGAGAG CTTCATTAGTAG CCAAGAT	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q61123 MATERNAL EMBRYONIC MESSAGE 3 (MEM3) - MUS MUSCULUS (MOUSE), 754 aa.	0.00E+00	16 (12q12)
165	cg43980521	1011	GCGCATGGGTC CCTCCAGGAAG GCTT[G/G]GTTA GAGTCCCAGGG TGGTCCCCA	T	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA20795 KIAA0337 PROTEIN - HOMO SAPIENS (HUMAN), 1510 aa.	0.00E+00	11
166	cg43980521	551	CCCTCAGCTTG GGGGTCTCTC CT[G/A]AAGGG CTTCCCTTGGCA GAAGGG	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA20795 KIAA0337 PROTEIN - HOMO SAPIENS (HUMAN), 1510 aa.	0.00E+00	11
167	cg43980521	873	AGCATCTTGATC TAGAGGACTGA GG[G/A]CAGCCC CATCAGGCTGG GGCCCTGG	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA20795 KIAA0337 PROTEIN - HOMO SAPIENS (HUMAN), 1510 aa.	0	11
168	cg44019839	3287	AGCTACACAGA GGAAATAACTTA GGT[C/G]ACTTCT GTTTTTTTAAAA AAAATA	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:Q99743 NEURONAL PAS DOMAIN PROTEIN 2 (NEURONAL PAS2) (MEMBER OF PAS PROTEIN 4) (MOP4) - Homo sapiens (Human), 824 aa.	0	

169	cg44021891	787	AGAAGACCTGG CTTCCTTACAAC AG[G/A]GACAGG CTGGTGGCTGG GGCTAGAG	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q92560 BRCA1 ASSOCIATED PROTEIN 1 (MYELOBLAST KIAA0272) - HOMO SAPIENS (HUMAN), 729 aa.	0	3
170	cg44021891	869	GCCCCCAGCTA GGACCCCTGTAG TTG[G/A]GACCG TGGCATGATACA AGGACCTG	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q92560 BRCA1 ASSOCIATED PROTEIN 1 (MYELOBLAST KIAA0272) - HOMO SAPIENS (HUMAN), 729 aa.	0	3
171	cg44921773	2876	TTCTGAGACAG GGTCTTGCTCT GTC[G/A]CCCAG GCTGGAGTGCA ATGGCACGA	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q13471 REPLICATION CONTROL PROTEIN 1 - HOMO SAPIENS (HUMAN), 861 aa.	0	1
172	cg44921773	2955	GGGCTCAAGTG ATCCTCCACCT CA[A/G]CCTCCC GAGTAGCTGAG ACTACAGG	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q13471 REPLICATION CONTROL PROTEIN 1 - HOMO SAPIENS (HUMAN), 861 aa.	0	1
173	cg43961485	650	GGTCTCCTCAG TGGTCTATTTTA GGT[G/G]GTGGTT TTTTTTTTTTTT TTACTG	T	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O60398 TXBP151 - HOMO SAPIENS (HUMAN), 563 aa.	1.5E-303	7
174	cg43985955	2111	GAGCACAGATA CAGTTTATGTAA CT[T/A]GATGGA AGAAAAATGGAAT TACTCCA	T	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q13492 CALM (TYPE I CALM PROTEIN) - HOMO SAPIENS (HUMAN), 652 aa.	2.7E-299	
175	cg44916647	1142	GCTCAGCAGCC CCTAGGAAAGTTA AG[C/T]GAGAGC TACAGGGCAGG GGGGCTCC	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O75057 KIAA0469 PROTEIN - HOMO SAPIENS (HUMAN), 539 aa.	4.3E-299	1

176	cg44916647	494	TCTGTACATGTA ACATGTGGCCA TG[C/gap]CCAGG CATCCAGCAT CTATCCTGA	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O75057 KIAA0469 PROTEIN - HOMO SAPIENS (HUMAN), 539 aa.	4.3E-299	1
177	cg44021459	2082	GGTCACTGTTTC CTCGGCATCGT GCT[C]GCCTGG AGAGAACTCCC GACCGGGA	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAC16046 FIP2 - HOMO SAPIENS (HUMAN), 577 aa.	1E-297	
178	cg43926814	372	TAGAAATTTCTA TCCCCCCCCATT T[C/T]TCCAGTAA TAAAAGTAGTG CTGGG	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW- ACC:Q13573 NUCLEAR PROTEIN SKIP (SNW1 PROTEIN) (NUCLEAR RECEPTOR COACTIVATOR NCOA- 62) - Homo sapiens (Human), 536 aa.	5E-289	14
179	cg43926814	412	GTAGTGCTGGG ATCTGGCACCC AGA[T/C]TTGGTT TTTATCCTGACC ATTACA	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW- ACC:Q13573 NUCLEAR PROTEIN SKIP (SNW1 PROTEIN) (NUCLEAR RECEPTOR COACTIVATOR NCOA- 62) - Homo sapiens (Human), 536 aa.	5E-289	14
180	cg43931431	1415	AGCCATGTACG TGAAATTGCTTG GG[A/T]ACCTGA ACTCCCGCTGG AATTTCTA	A	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:Q14154 HYPOTHETICAL PROTEIN KIAA0141 - Homo sapiens (Human), 515 aa.	7.2E-281	5
181	cg44031765	277	ATGCACCTGGC CCACATGGCTG GGC[G/A]CTGCA GCCTGCACTCC ACTCCAGG	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q14776 LZTR-1 - HOMO SAPIENS (HUMAN), 552 aa.	4.6E-279	22
182	cg44031765	4030	CATCTTTATAGG CCACCACTGTG TG[C/T]TTGCTG CGCCGGGCACC CACGAACT	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q14776 LZTR-1 - HOMO SAPIENS (HUMAN), 552 aa.	4.6E-279	22

183	cg43970492	331	TGCTTTGTTGCT TCAAGATGCATG C[A/C]CATCCTG GCCTTAGTGTC AAGTAT	A	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:P78395 PREFERENTIALLY EXPRESSED ANTIGEN OF MELANOMA - HOMO SAPIENS (HUMAN), 509 aa.	3.60E-270	22
184	cg42847874	1118	ACAAAAATTAGC CGGGCATGGTG GC[G/A]CACGCC TGTAGTCCCAG CTACTTAG	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA34492 KIAA0772 PROTEIN - HOMO SAPIENS (HUMAN), 468 aa.	6.30E-258	20
185	cg43951020	534	GAGTGCAGTGG CTCACTGCAAC CTC[C/T]GCCTC CCAGGTTCAAG CAATTCTCC	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O76021 PBK1 PROTEIN - HOMO SAPIENS (HUMAN), 516 aa.	6.60E-255	
186	cg43951020	552	CAACCTCGCC TCCCAGGTTCAA GC[A/G]ATTCTC CTGCCCTCAGCC TCCCTAGT	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O76021 PBK1 PROTEIN - HOMO SAPIENS (HUMAN), 516 aa.	6.60E-255	
187	cg43971614	2720	ACCATTGCTTTG GTCAATTCAACC T[G/A]GGGGGAA AAGAGTCAAATA TGTCCA	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q13283 GAP SH3 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 466 aa.	5.30E-253	5
188	cg43971614	2802	CTCTGCACCAC AGCACCGAGGA TAG[T/C]ACAAA CCCCTCACGGC TCTGCGTCC	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q13283 GAP SH3 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 466 aa.	5.30E-253	5
189	cg43962954	192	CGGGCTCCCCA TGCAGCCCTAG AGA[C/gap]GGG AGAAGTCCAGT GTGCTGTTCCA	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O75455 HERPESVIRUS ENTRY PROTEIN B - HOMO SAPIENS (HUMAN), 479 aa.	4.80E-252	19

190	cg43917689	1684	AGGCAACACCT GTGGAGGAAGG GCA[C/T]GGGGC AAAAGCTCACCT CAGAAAGTG	C	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q92551 MYELOBLAST KIAA0263 - HOMO SAPIENS (HUMAN), 441 aa.	3.50E-240	3
191	cg43916785	2176	TCAGATGACTTT ACAACCAAGGG AG[T/C]ACACAG GGCAACAACAA ATTAGAGG	T	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAC97961 S164 - HOMO SAPIENS (HUMAN), 735 aa (fragment).	2.50E-230	14
192	cg43287642	307	GCAACTATT AAAACCCAAAG GA[G/A]AAAGGA TGGTACTACCAT AAATCAC	G	A			SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD20347 NEBULIN - HOMO SAPIENS (HUMAN), 977 aa (fragment).	3.50E-224	
193	cg43986954	1072	AGTGAACATT TTTGTTCATTT C[T/C]AGGAATTT TCTCTGGGGA AAGTCG	T	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAC68871 METHYL-CPG BINDING PROTEIN MBD2 - HOMO SAPIENS (HUMAN), 411 aa.	9.40E-224	18
194	cg42882543	3078	TCCCGAGTAGC TGGGATTACAG GCA[T/C]GCGCC ACCACGCCAG CTAATTTTT	T	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O75177 KIAA0693 PROTEIN - HOMO SAPIENS (HUMAN), 404 aa (fragment).	2.30E-220	
195	cg43062833	1567	TGAAAAGTATTA TGGAAATCACTG C[A/T]GCACAGG AAAAGTAATTCA GATGTT	A	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW- ACC:Q93088 BETAINE- HOMOCYSTEINE S- METHYLTRANSFERASE (EC 2.1.1.5) - Homo sapiens (Human), 406 aa.	2.10E-219	5
196	cg43959148	342	AGACTAGTGTG GGCCTTGGGCC CCC[C/gap]TCAT TTTGACATCCTT CCAGATGGT	C	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O75955 FLOTILLIN-1 - HOMO SAPIENS (HUMAN), 427 aa.	1.40E-215	6

197	cg43950766	385	GTTACATTTAG TGAACCTGCATT T[C/gap]ATGGGG GGGGGGGGG TACACAGTA	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD4491 PTD004 - HOMO SAPIENS (HUMAN), 396 aa.	5.30E-214	22
198	cg43958860	1340	TCTGTCITTTAT TTAACAAAAAT GTT/CJAATTAAT GTAAACITGGAA TCAAG	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:P48745 NOV PROTEIN HOMOLOG PRECURSOR (NOVH) - Homo sapiens (Human), 357 aa.	6.00E-206 (8q24.1)	8
199	cg43968205	1516	CTATAGCAGAG GGGGTTATGGG GGC[G/A]GGAGG GTAGACTGACAT ACAGAAAT	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB46373 HYPOTHETICAL 71.0 KD PROTEIN - HOMO SAPIENS (HUMAN), 653 aa (fragment).	6.90E-206	
200	cg43950996	825	ACGCCAGTCCA GAAAGAAGGTG CTG[G/A]AGCCC CTGCTCTGTCCT CTCCATCA	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:P78545 ESE-1B - HOMO SAPIENS (HUMAN), 371 aa.	6.20E-204	1
201	cg44924222	1787	TAAGGGTGAGC AGCAGCAGGAG CGC[A/T]TTGAA GAAGAAAGTAGA AGGGGATGT	A	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW- ACC:P27539 EMBRYONIC GROWTH/DIFFERENTIATION FACTOR 1 PRECURSOR (GDF-1) - Homo sapiens (Human), 372 aa.	2.7E-203	
202	cg44924222	1834	ATGTCAGGCAC CGTGCGCAGAC TGC[A/G]GTGAC TGGTGGCATA AGGACCTTG	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW- ACC:P27539 EMBRYONIC GROWTH/DIFFERENTIATION FACTOR 1 PRECURSOR (GDF-1) - Homo sapiens (Human), 372 aa.	2.7E-203	
203	cg44924222	2073	GTACCGGAAGG CGTAGGAGGAG ACG[A/G]TGAGG ATGAGAGTGAC CACGTGGTG	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW- ACC:P27539 EMBRYONIC GROWTH/DIFFERENTIATION FACTOR 1 PRECURSOR (GDF-1) - Homo sapiens (Human), 372 aa.	2.7E-203	

204	cg44916575	1943	GAGGACAAAA CAGAAAGCCCT GTG[AT]GTGTG GGAAACTCCG CTGCAGAGA	A	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q16842 BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE (EC 2.4.99.4) (CMP-N- ACETYLNEURAMINATE-BETA- GALACTOSAMIDE-ALPHA-2,3- SIALYL- TRANSFERASE) - HOMO SAPIENS (HUMAN), 350 aa.	3.7E-197	
205	cg42650960	2321	GGCTGGAGTGC AGTGGCAGCAT CTC[G/A]GCTCA CTGCAAGCCTC CGCCTCCCG	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:Q10981 GALACTOSIDE 2-L- FUCOSYLTRANSFERASE 2 (EC 2.4.1.69) (GDP-L-FUCOSE:BETA- D- GALACTOSIDE 2-ALPHA-L- FUCOSYLTRANSFERASE 2) (ALPHA(1,2)FT 2) (FUCOSYLTRANSFERASE 2) (SECRETOR BLOOD GROUP ALPHA-2- FUCOSYLTRANSFERASE) (SECRETOR FACTOR) (SE) (SE2) - Homo.sapiens (Human), 343 aa.	2E-189	
206	cg43947129	2163	CTGGGGGCGTC CATGGTCCGGC GGC[G/C]AGGGC GGTGAGTCAGC CAAGGAGGA	G	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:P10658 PROBABLE PHOSPHOSERINE AMINOTRANSFERASE (EC 2.6.1.52) (PSAT) (ENDOMETRIAL PROGESTERONE-INDUCED PROTEIN) (EPIP) - Oryctolagus cuniculus (Rabbit), 370 aa.	3E-188	
207	cg43922383	199	ATCTGAAAATGG TGTGTGGCGTC GC[G/A]CGCGCC AGCTATCGTCA GTGCCITT	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q15435 YEAST SDS22 HOMOLOG - HOMO SAPIENS (HUMAN), 360 aa.	7.3E-185	2
208	cg43922383	222	CGCGGCCAGC TATCGTCAGTGC CT[gap/G]TTATT GCCATTGGGTTT GTGACTGT	gap	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q15435 YEAST SDS22 HOMOLOG - HOMO SAPIENS (HUMAN), 360 aa.	7.3E-185	2

209	cg43922383	239	TCAGTGCCTTTA TTGCCATTGGGT T[T/gap]GTGACT GTTGATATAGTG ACGACCT	T	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q15435 YEAST SDS22 HOMOLOG - HOMO SAPIENS (HUMAN), 360 aa.	7.3E-185	2
210	cg43922383	250	ATTGCCATTGG GTTTGTGACTGT TG[A/G]TATAGT GACGACCTCAG GAGCAACA	A	G			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q15435 YEAST SDS22 HOMOLOG - HOMO SAPIENS (HUMAN), 360 aa.	7.3E-185	2
211	cg43922383	263	TTGTGACTGTTG ATATAGTGACGA C[C/G]TCAGGAG CAACAGGTGGG TTAAAAA	C	G			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q15435 YEAST SDS22 HOMOLOG - HOMO SAPIENS (HUMAN), 360 aa.	7.3E-185	2
212	cg43953935	458	CTTTTAAATAA ATGACTGCGAG TG[A/G]GTGTAA ATTCTGAGAAAA TTACATT	A	G			SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD41634 LYSOSOMAL TRAFFICKING REGULATOR 2 - MUS MUSCULUS (MOUSE), 703 aa (fragment).	2.4E-177	13
213	cg43933591	1167	ACATTGGAATT TTAGCTTTTTTTT [T/gap]GCCTCTC TACTGTGTCACT AAATAT	T	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q18476 C35A5.8 - CAENORHABDITIS ELEGANS, 1078 aa.	1.70E-176	8
214	cg43949875	2329	CTGAGTAGCTG GGATTACAGGC GTG[T/C]GCCAC CATGCCACGCT AATTTTTTG	T	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34394 NUCLEAR PORE COMPLEX INTERACTING PROTEIN NPIP - HOMO SAPIENS (HUMAN), 350 aa.	6.60E-175	
215	cg43100840	1131	GGACAGGGGTG CAGCTGGCAGC CGA[G/A]AAAGG GGACCACCTCG GAGGGCTGG	G	A			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:P49752 HYPOTHETICAL PROTEIN ZAP113 - Homo sapiens (Human), 309 aa (fragment).	3.20E-168	

216	cg43922270	2077	TGTATATGTGTA CGTAGGTAGAT GT[G/A]TGCAGC ATGCGGCAGGT TTGCCAGG	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:Q14140 HYPOTHETICAL PROTEIN KIAA0127 - Homo sapiens (Human), 314 aa.	1.30E-162	2
217	cg43993462	1461	CAGATGAGCT GCAGAGGTTTC CTC[C/T]CTGCTT TACAATCCCTTA TTGAAGT	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q63965 TRICARBOXYLATE CARRIER - RATTUS NORVEGICUS (RAT), 357 aa (fragment).	5.10E-161	5
218	cg43993462	384	TAAACATCTACA GAGTTGAAACAT A[A/C]TCTGTGCAT ATTAAATATATT ATCTA	A	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q63965 TRICARBOXYLATE CARRIER - RATTUS NORVEGICUS (RAT), 357 aa (fragment).	5.1E-161	5
219	cg43993462	624	TAGTCTCACITC TTACCAAAAAA A[A/gap]CAATGA ACTGGATTGAG CCCACTCA	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q63965 TRICARBOXYLATE CARRIER - RATTUS NORVEGICUS (RAT), 357 aa (fragment).	5.1E-161	5
220	cg43329741	996	GCAGTGCAGGA GATGACAGAGT GAG[G/A]AGGGC CCAGAGCAGAA TTCTGGCCC	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD39906 FH1/FH2 DOMAIN- CONTAINING PROTEIN FHOS - HOMO SAPIENS (HUMAN), 1164 aa.	6.7E-159	
221	cg42910688	1687	AAACAATTTTG TTCAATGCCAC C[G/A]AGACATA TAGAATTGGAA CTGATA	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:P55040 GTP-BINDING PROTEIN GEM (GTP-BINDING MITOGEN-INDUCED T-CELL PROTEIN) (RAS-LIKE PROTEIN KIR) - Homo sapiens (Human), 296 aa.	7.7E-158	8
222	cg43967474	969	TGCTGGGACC ATGGATGGGA GGA[G/gap]GGG CACAGGGCCCA GTGCAGATGAA	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA76848 KIAA1004 PROTEIN - HOMO SAPIENS (HUMAN), 496 aa (fragment).	1.70E-152	11

230	cg43920176	2819	AAAGCTGCTTTG TTAGGTTCCCTTA T[G/T]TTTTATTA ACTGTCTTTTCT CAGTT	G	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD28325 LUMAN2 - HOMO SAPIENS (HUMAN), 272 aa.	1.40E-140	
231	cg43920176	2909	ATTTGTCAATTT TTTACATCAACT T[C/T]ATGTGCTTT GTTTTTACATGG TAATT	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD28325 LUMAN2 - HOMO SAPIENS (HUMAN), 272 aa.	1.40E-140	
232	cg43950100	856	CAAAATTAACAA ATTCACAAAATA C[A/G]ACAGCTA GAATTACAAAT CCATTC	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O14681 PIG8 - HOMO SAPIENS (HUMAN), 318 aa.	1.70E-139	11
233	cg43950100	952	GGCACAGGGAG AAAAACAAAAGTG TT[C/gap]CAATC AGTCCAGGCAC AGGGACTGG	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O14681 PIG8 - HOMO SAPIENS (HUMAN), 318 aa.	1.70E-139	11
234	cg43950100	391	ACATTGACCCCT TCAGTTCCTATA T[G/A]CAGCACC CAATATTCCTTT GAAATA	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O14681 PIG8 - HOMO SAPIENS (HUMAN), 318 aa.	1.70E-139	11
235	cg43950100	515	CAGGTTTAGTGT TGTTGTAGTGG CA[C/T]TTGTCCA GAATTGGTACCT CCCCAT	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O14681 PIG8 - HOMO SAPIENS (HUMAN), 318 aa.	1.70E-139	11
236	cg43132640	1317	CTCTATGAACCTC TGTTTCTTTTCT A[A/gap]TGAGAT ATTAAACCATGT AAAGAAC	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:P11226 MANNOSE-BINDING PROTEIN C PRECURSOR (MBP-C) (MBP1) (MANNAN-BINDING PROTEIN) (MANNOSE-BINDING LECTIN) - Homo sapiens (Human), 248 aa.	4.20E-134 (10q11.2)	10

237	cg44938448	1310	TGAAAGTTAGAGT AGCTGCAAATCT CTT/gapJTAAGTA TCAATGTAAAGA AGCAGAT	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75035 KIAA0447 PROTEIN - HOMO SAPIENS (HUMAN), 254 aa.	4.80E-129	1
238	cg44938448	511	AATGCCACTTTC AGATGGAAGGG AA[A/G]TGAGAT GGAAAACAACA AAAAAGGA	G			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75035 KIAA0447 PROTEIN - HOMO SAPIENS (HUMAN), 254 aa.	4.80E-129	1
239	cg43949897	923	AGCACTTTGGA GCTGGCCTCGC CCC[C/gap]TAGG AGGAGAGGGTC CCTCCTGGGT	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O60499 SYNTAXIN 10 - HOMO SAPIENS (HUMAN), 249 aa.	1.80E-126	19
240	cg42549778	1067	GGGGTGTCTCC TGGAAGCCCCA AGA[G/C]CATCC AGGATTGCCTC CCAGCTGOC	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD29690 PUTATIVE ZINC FINGER TRANSCRIPTION FACTOR OVO1 - MUS MUSCULUS (MOUSE), 267 aa.	3.70E-126	
241	cg44028574	990	CAGCTCCCAGC TACCATGATGAG CC[C/gap]TGGC GGCTTGAGCAC AGTGAGTGCT	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD27724 CGI- 15 PROTEIN - HOMO SAPIENS (HUMAN), 329 aa.	4.00E-122	20
242	cg44035718	1088	TCTCATCTAGTG CTGAAGTCTGA GG[G/A]CTCTGC AGCATCAGACC CACCTCTA	A			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:BAA83010 KIAA1058 PROTEIN - HOMO SAPIENS (HUMAN), 1534 aa (fragment).	2.20E-121	2

243	cg44035718	1172	GAAGAGAAAGA TAGGTTTAATTT ATT[C]TGAAGTT TTCATGGTGTTA ATATTT	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:BAA83010 KIAA1058 PROTEIN - HOMO SAPIENS (HUMAN), 1534 aa (fragment).	2.20E-121	2
244	cg43963595	1212	CCCCCGCAGAC AGAGCCCGGAG GCT[T/G]TCTGG TGCAGCGATGT TTAATGGCA	T	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75391 SPERM ACROSOMAL PROTEIN - HOMO SAPIENS (HUMAN), 293 aa.	8.50E-120	17
245	cg43963595	1213	CCCCGCAGACA GAGCCCGGAGG CTT[T/G]CTGGT GCAGCGATGTT TAATGGCAA	T	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75391 SPERM ACROSOMAL PROTEIN - HOMO SAPIENS (HUMAN), 293 aa.	8.50E-120	17
246	cg43963595	1402	ATGTTACAGTAT GTACAAAGACCC CT[C/gap]CCCTC GGGGACGGG GCGGACTCCG	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75391 SPERM ACROSOMAL PROTEIN - HOMO SAPIENS (HUMAN), 293 aa.	8.50E-120	17
247	cg43992566	492	AAATAGAGAATC CAGACCCCTTCC CA[G/A]ATAATTT AAGAACTGAGTT TTCCTC	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:O14530 PROTEIN 1-4 - Homo sapiens (Human), 226 aa.	5.40E-118	
248	cg43992566	670	ATTTAAATCTGA AGCAGAAAAAAA A[A/gap]GACAAT TTACAAAGAAAT ATTGAGC	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:O14530 PROTEIN 1-4 - Homo sapiens (Human), 226 aa.	5.40E-118	
249	cg43067745	907	TCCCTGCACGC CTTTACGTCAGA CT[G/A]TCACCA CAAGAGCCTTG AGTGTCCA	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75839 TSC501 PROTEIN - HOMO SAPIENS (HUMAN), 227 aa.	6.90E-118	

250	cg42697161	552	ACGTGGTGTCTG GTAGTGTCTTGT TG[A/G]GTGTGA ATTCTCTCTCAT ACAAAAG	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O15262 RING FINGER PROTEIN - HOMO SAPIENS (HUMAN), 247 aa.	1.00E-114	4
251	cg43957889	1466	GTGCAATGGCA TGATCTCGGCT CAC[C/T]GCAAC CTCTGCCTCCC GGGTTCAAG	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O00577 COSMID 6E5 CDK4, SAS AND KIAA0167 GENES, COMPLETE CDS, AND OS9 - HOMO SAPIENS (HUMAN), 227 aa.	2.70E-111	12
252	cg42391024	404	AACTGCAGACA AATTTCAAATT CA[C/A]TTCCTTA CTTCTCCAAGAT CTTCGA	C	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:O43583 DRP1 PROTEIN (DRP) - Homo sapiens (Human), 243 aa.	4.30E-109	
253	cg43976566	711	CTTTAATGAAAC ACTTTGGATCGT C[A/G]GTGCTGA AGTGAAAAGAAAT GTGCTG	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:BAA74894 KIAA0871 PROTEIN - HOMO SAPIENS (HUMAN), 469 aa.	1.70E-107	4
254	cg44001900	936	GATGCTAAAG CTTCTGCCGAAAT GT[G/A]TTCACG TTTAATGTTGGG AAATCCC	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:BAA83057 KIAA1105 PROTEIN - HOMO SAPIENS (HUMAN), 730 aa (fragment).	1.20E-104	
255	cg43954569	471	TCAGCCCCACAT GACTCAGGGAC AC[A/gap]CTCCC CAGCGGTTGCT GGAGGCACC	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:P78560 DEATH DOMAIN CONTAINING PROTEIN CRADD (CASPASE AND RIP ADAPTATOR WITH DEATH DOMAIN) (RIP ASSOCIATED PROTEIN WITH A DEATH DOMAIN) - Homo sapiens (Human), 199 aa.	1.40E-101	12
256	cg43925519	791	AGTGGCCCTT TCCCGCCCTGA AGA[T/C]GTTTCA CACGAAAAGGC CGTTTGT	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:P78317 ZINC FINGER PROTEIN - HOMO SAPIENS (HUMAN), 190 aa.	4.40E-100	4

257	cg43145684	711	TGGCAAACTG CCAGCAGCGGT TGC[C]TGAAAA TGCTGGGTTGG GTGCCTACT	C	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:BAA81666 DNA POLYMERASE ETA - HOMO SAPIENS (HUMAN), 713 aa.	2.90E-99	
258	cg43981803	626	ACCAGCTCGGA GAGGGCACTTG AGA[G]TGGTCT ATGAACAAATCT GTCTAAAA	G	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q16635 TFAZZIN - Homo sapiens (Human), 292 aa.	7.1E-97	X
259	cg44006111	1906	AGCCTGATGC ACATGTGCACA GGT[A]GJCCTAC ATGCTCTGTTCT TGTCACACA	A	G			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to REMTREMBL- ACC:G1100182 T-CELL RECEPTOR BETA - HOMO SAPIENS (HUMAN), 311 aa.	3.8E-95	
260	cg44924968	1363	TGCCAGGGAC CTGAGCCCGAG ACA[C]TCCCTG CATTGTATCCAA CCAGGTCA	C	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:AAD43192 WUGSC:H_DJ0726N20.1 PROTEIN - HOMO SAPIENS (HUMAN), 191 aa (fragment).	6.8E-95	7
261	cg44924968	1364	GGCCAGGGACC TGAGCCCGAGA CAC[C]TCCCTGC ATTGATCCAAC CAGGTCAG	C	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:AAD43192 WUGSC:H_DJ0726N20.1 PROTEIN - HOMO SAPIENS (HUMAN), 191 aa (fragment).	6.80E-95	7
262	cg43977021	1080	TGTCATCTAAAG TAATTCATTAAT GTTAACAGGAG TAGATGAGGCC TGGCACA	T	A			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q14206 ZAKI-4 MRNA IN HUMAN SKIN FIBROBLAST, COMPLETE CDS - HOMO SAPIENS (HUMAN), 192 aa.	9.20E-91	6
263	cg43977021	1087	TAAAGTAATTCA TTAATGTACAGG A[G/A]TAGATGA GGCCTGGCACA CATAGCA	G	A			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q14206 ZAKI-4 MRNA IN HUMAN SKIN FIBROBLAST, COMPLETE CDS - HOMO SAPIENS (HUMAN), 192 aa.	9.20E-91	6

264	cg43977021	1098	ATTAATGTACAG GAGTAGATGAG GC[CT]TGGCAC ACATAGCAGAA GGTAATGG	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q14206 ZAKI-4 MRNA IN HUMAN SKIN FIBROBLAST, COMPLETE CDS - HOMO SAPIENS (HUMAN), 192 aa.	9.20E-91	6
265	cg43977021	1107	CAGGAGTAGAT GAGGCCTGGCA CAC[A/G]TAGCA GAAGGTAATGG TTCTATAGG	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q14206 ZAKI-4 MRNA IN HUMAN SKIN FIBROBLAST, COMPLETE CDS - HOMO SAPIENS (HUMAN), 192 aa.	9.20E-91	6
266	cg43977021	1116	ATGAGGCCTGG CACACATAGCA GAA[G/A]GTAAT GGTCTATAGGT GTATCTTC	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q14206 ZAKI-4 MRNA IN HUMAN SKIN FIBROBLAST, COMPLETE CDS - HOMO SAPIENS (HUMAN), 192 aa.	9.20E-91	6
267	cg43977021	1169	TAATGCACCTTG GGCTAGAGAAA TA[G/C]AAAAATC ACACGTAACAAA AACAAA	G	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q14206 ZAKI-4 MRNA IN HUMAN SKIN FIBROBLAST, COMPLETE CDS - HOMO SAPIENS (HUMAN), 192 aa.	9.20E-91	6
268	cg43999373	303	CACAGAAATTCAG AACTTTTTCACC C[G/C]GAACTGG AGAAGGAGCAC TCCGTCA	G	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O88994 HYPOTHETICAL 38.2 KD PROTEIN - RATTUS NORVEGICUS (RAT), 338 aa.	1.50E-89	1
269	cg43980889	915	TTTGAGAGCTG CAGCAGAAGCG GCT[G/T]TATCA CAGACTGGATTT AGTTATGA	G	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O00581 HYPOTHETICAL 20.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 176 aa.	4.5E-89	
270	cg43980889	936	GGCTGTATCAC AGACTGGATTTA GT[T/G]ATGATG AAAATACTGGAC TGTAATT	T	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O00581 HYPOTHETICAL 20.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 176 aa.	4.5E-89	

271	cg44030196	611	TAGATTGTTCCAG TACTCAGCTCAC C[A/gap]CCCATA AGACCATTTCTC CTCTGCG	A	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:AAD40853 SIRTUIN TYPE 5 - HOMO SAPIENS (HUMAN), 310 aa.	7.4E-89	
272	cg40336929	317	GGCAACAAGTT ACAGCGGCGGG AGATT[A]GTTCTT TCTCTCACCTGC CGGGGGG	T	A			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O73884 PUTATIVE PHOSPHATASE - GALLUS GALLUS (CHICKEN), 268 aa.	3.4E-84	
273	cg43920571	684	AGAAGACAGCG CGCAGAAATAG TGC[G/A]GAGAG AAATGACCAGTA CTATTTAT	G	A			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P34624 HYPOTHETICAL 63.5 KD PROTEIN ZK353.1 IN CHROMOSOME III - Caenorhabditis elegans, 548 aa.	3.5E-82	10
274	cg43958980	537	TAAGATCCTCCA TCCCACCAAAAA T[A/G]ACCCACA ATGACTCCAAAT CTTGTT	A	G			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:CAB43239 HYPOTHETICAL 41.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 383 aa (fragment).	4.50E-82	6
275	cg43320682	512	CATTGGCAACG GCTGCCCACTA GGG[G/gap]CAC TGCCACTTGCCCT GGCTCAAACT	G	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:CAB45773 HYPOTHETICAL 18.0 KD PROTEIN - HOMO SAPIENS (HUMAN), 162 aa (fragment).	6.60E-81	
276	cg42708544	845	CCAGGCTTGCC TCTAGATTGGCT GG[G/gap]CCAG AATTTCTGGGGT CAGTCTGAA	G	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O14684 PIG12 - HOMO SAPIENS (HUMAN), 153 aa.	2.60E-79	
277	cg43949796	637	GGGAAGTAAAA TGAAGGAAGCA GAC[C/T]TCTTG CTCATCTTTCCA AATGAAAT	C	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q94547 RGA AND ATU GENES, COMPLETE CDS - DROSOPHILA MELANOGASTER (FRUIT FLY), 579 aa.	1.20E-75	12

278	cg43298234	843	TAAGGCCAGAG CTTGTGTGCTG GGC[A/gap]CAGA AATCACCTGCTG CATCCTGTG	A	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60896 MRNA ENCODING RAMP3 PRECURSOR - HOMO SAPIENS (HUMAN), 148 aa.	1.30E-75	7
279	cg43926358	607	CAGTGATGTGC TGGCCCTTTCA GGG[A/C]CACAG GCCCTTCAGC TTCACCGGA	A	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75272 R33729_1, PARTIAL CDS - HOMO SAPIENS (HUMAN), 152 aa (fragment).	1.90E-74	19
280	cg35060315	1328	CCAAACTATCTC ACCCCTACCCTC CC[T/C]AGGATC CACTTCITTTGA ATGACAA	T	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P01225 FOLLITROPIN BETA CHAIN PRECURSOR (FOLLICLE- STIMULATING HORMONE) (FSH-B) - Homo sapiens (Human), 129 aa.	9.50E-73	11
281	cg35060315	1540	CTATTTTATCCA TCCATGTTCTCC C[A/gap]AATCTG TGCTTTCTTTCA ACAGGTT	A	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P01225 FOLLITROPIN BETA CHAIN PRECURSOR (FOLLICLE- STIMULATING HORMONE) (FSH-B) - Homo sapiens (Human), 129 aa.	9.50E-73	11
282	cg35060315	1542	TTTTATCCATCC ATGTTCTCCCAA A[gap/A]TCTGTG CTTCTTTTCAAC AGGTTAT	gap	A			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P01225 FOLLITROPIN BETA CHAIN PRECURSOR (FOLLICLE- STIMULATING HORMONE) (FSH-B) - Homo sapiens (Human), 129 aa.	9.5E-73	11
283	cg35060315	1557	GTTCTCCCAAT CTGTGCTTTCTT T[C/T]AACAGGTT ATATATTAAAC TATTT	C	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P01225 FOLLITROPIN BETA CHAIN PRECURSOR (FOLLICLE- STIMULATING HORMONE) (FSH-B) - Homo sapiens (Human), 129 aa.	9.5E-73	11
284	cg35060315	1562	CCCAATCTGTG CTTCTTTTCAAC A[G/C]GTTATATA TTAAACTATTT CATGA	G	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P01225 FOLLITROPIN BETA CHAIN PRECURSOR (FOLLICLE- STIMULATING HORMONE) (FSH-B) - Homo sapiens (Human), 129 aa.	9.5E-73	11

285	cg44126579	18	TGTACAACTGAT TAGAG[A/gap]GT TTTTTTTTCTTT TTCTTTTCAA	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:P90839 F16A11.1 - CAENORHABDITIS ELEGANS, 673 aa.	1.1E-71	16
286	cg43951096	719	CCTCTCCTCCAA GAGTTGGTTCC GC[A/gap]AGAG GTGAAAGAAC TCTCAATAGT	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q23382 ZK1058.4 - CAENORHABDITIS ELEGANS, 442 aa.	2E-71	17
287	cg43951096	884	CACAGCCATAAT ATAGAGAACAG AG[C/gap]TTCTC CATGAACATCCA CCAGGCTG	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q23382 ZK1058.4 - CAENORHABDITIS ELEGANS, 442 aa.	2E-71	17
288	cg43960676	65	AGCAGCCAGCT TCATTGGCTGCA AA[C/T]GCCTCT CTCAGGTGAGT CAAAGGAG	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:AAD43443 26S PROTEASOME SUBUNIT P40.5 - MUS MUSCULUS (MOUSE), 376 aa.	5.3E-69	
289	cg43323149	1101	TCACCTCAGATG AGTGTGGCTCC CC[C/G]CGCTCC CATACTGCAGC CTGCCCCCT	C	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P50636 GAMETOGENESIS EXPRESSED PROTEIN GEG-154 - Mus musculus (Mouse), 429 aa.	1E-68	1
290	cg43969533	364	AAGGGAAGCCT ATCCTATTTTTTT TT[gap]TCCTTT GCGAAACACAGA AGCCAAAGT	T	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:AAD39844 HSPC028 - HOMO SAPIENS (HUMAN), 419 aa.	1.6E-67	7
291	cg43969533	365	AGGGAAGCCTA TCCTATTTTTTTT TT[gap]CCTTTG CGAAACACAGAA GCCAAGTT	T	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:AAD39844 HSPC028 - HOMO SAPIENS (HUMAN), 419 aa.	1.6E-67	7

292	cg39376027	601	CCGGGGAGGTG GTTCTGGTAATC TG[G/T]GGGGA GCCGGGACAGG CGCCCCGA	G	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:AAD39515 HERMES - MUS MUSCULUS (MOUSE), 197 aa.	2.3E-66	
293	cg39376027	604	GGGAGGTGTT CTGGTAATCTG GGG[G/T]GGAGC CGGGACAGGCG CCCCGAGTT	G	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:AAD39515 HERMES - MUS MUSCULUS (MOUSE), 197 aa.	2.3E-66	
294	cg43976681	210	CTCTCTCTTCGC CGCCGACGCAG AA[A/G]GGAGCT GGGGAGGAAAA AGCTGCTG	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:AAD29427 MYOMEGALIN - RATTUS NORVEGICUS (RAT), 2324 aa.	4.3E-66	11
295	cg43085556	131	GTAAGGTAATAAT GTGAATCAATAT GT[C/T]AGTTCT GGGCAATTATTC TGCAAA	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60223 SSX3 - HOMO SAPIENS (HUMAN), 188 aa.	8.8E-65	
296	cg43085556	149	CAATATGTTAGT TCTGGGCAATTA TT[C/T]CTGCAAAAT TCTGCCAGATAA TTAAA	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60223 SSX3 - HOMO SAPIENS (HUMAN), 188 aa.	8.8E-65	
297	cg43085556	150	AATATGTTAGT CTGGGCAATTAT T[C/T]TGCAAAAT CTGCCAGATAAT TAAAG	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60223 SSX3 - HOMO SAPIENS (HUMAN), 188 aa.	8.8E-65	
298	cg43085556	30	TGTTGTTCTCA AGCTTTTCGCCT A[C/T]ATTTTGA CTAACCCCTGCTT ATTCC	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60223 SSX3 - HOMO SAPIENS (HUMAN), 188 aa.	8.8E-65	

299	cg43085556	45	TTTTGCCTACA TTTTAGACTAAC C[C/T]TGCTTATT CCTGTGAATCAA GTGGT	C	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60223 SSX3 - HOMO SAPIENS (HUMAN), 188 aa.	8.8E-65	
300	cg43085556	65	TAACCCCTGCTTA TTCCCTGTGAATC A[A/C]GTGGTGA TCTTCTGCAGCT TGGAAAT	A	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60223 SSX3 - HOMO SAPIENS (HUMAN), 188 aa.	8.8E-65	
301	cg43920089	437	GCAATTGCTGCT TGTCCTTGATTT T[G/A]TTTGGCT CAATCCCTTCCT GGCAGC	G	A			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O14716 DNAJ PROTEIN - HOMO SAPIENS (HUMAN), 135 aa.	2E-63	
302	cg43950850	263	AAACATGTTCCA TCAAATTCAGAA A[C/gap]AGCAGG TATCAGTGAAC TGGAGCA	C	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:O95298 NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-B14.5B) (CI-B14.5B) - Homo sapiens (Human), 119 aa.	7.8E-62	11
303	cg43950850	736	AGGAAAACAC GACGACCACTA CCC[G/C]GGCCT AAGCGGTCAGC TTTCTCCTC	G	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:O95298 NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-B14.5B) (CI-B14.5B) - Homo sapiens (Human), 119 aa.	7.8E-62	11
304	cg44128084	1012	CATCCGCGCTG ACGGCAGTCAC CGG[T/C]GAGAC CGGCGCCGAA AGACCATGG	T	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O33196 HYPOTHETICAL 32.9 KD PROTEIN - MYCOBACTERIUM TUBERCULOSIS, 307 aa.	1.7E-59	
305	cg43976473	984	GACGCTCGCTG TCCCCGAGGGC CCG[gap/C]TGC GCCGCCCTCGT GGTACGAATAC	gap	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O35946 HYPOTHETICAL 14.9 KD PROTEIN - RATTUS NORVEGICUS (RAT), 137 aa.	3.5E-59	11

306	cg44924858	546	GCTTCTGTCAGAG CGTTACTTTTCAC C[G/A]TGCCTGC TGTTTCCACAGG AAGAGT	G	A			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q12773 GUANINE NUCLEOTIDE REGULATORY PROTEIN - HOMO SAPIENS (HUMAN), 460 aa.	4.3E-59	
307	cg44924858	558	CGTTACTTTTCAC CGTGCCTGCTG TTT[C]CCACAG GAAGAGTCTGT CTGTTCCA	T	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q12773 GUANINE NUCLEOTIDE REGULATORY PROTEIN - HOMO SAPIENS (HUMAN), 460 aa.	4.3E-59	
308	cg44924858	755	ACCCAGCTTG CCCGGACAGCAC ACA[G]AACTG TTTCTTTGGCTT GACGAATA	A	G			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q12773 GUANINE NUCLEOTIDE REGULATORY PROTEIN - HOMO SAPIENS (HUMAN), 460 aa.	4.30E-59	
309	cg43961591	222	ACACCACTGGT ACTCACACCCC CTC[T/C]GGCTG GGTCTCTGGT GCGCCCTGC	T	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:O35414 STATHMIN-LIKE PROTEIN B3 (RB3) - Rattus norvegicus (Rat), 189 aa.	3.10E-58	
310	cg43924285	528	CTGCATATGTTT GCAGTTTTCAT C[A/G]ACTTCTTC ATAAACAAACAA ACATT	A	G			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:AAD29804 F26H11.12 PROTEIN - ARABIDOPSIS THALIANA (MOUSE- EAR CRESS), 323 aa.	4.20E-57	15
311	cg43924285	574	ACATTTTCTAGA AACC AAAATATG T[A/G]GTGGCCC AAAGGAGCTCTT AAGCAA	A	G			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:AAD29804 F26H11.12 PROTEIN - ARABIDOPSIS THALIANA (MOUSE- EAR CRESS), 323 aa.	4.20E-57	15
312	cg43958224	198	GTTTGATCCTCA GCCAGACGCA CA[G/A]GCCCTA CAAGATCCCA CCCTCCAA	G	A			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:CAB43298 HYPOTHETICAL 13.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 118 aa (fragment).	2.30E-53	19

313	cg43971060	502	AACGGCTTTAAA CACAAGCTCAG GG[G/gap]CTTG GGGTTTATCCC GAGGGCACAG	G	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P31639 SODIUM/GLUCOSE COTRANSPORTER 2 (NA(+)/GLUCOSE COTRANSPORTER 2) (LOW AFFINITY SODIUM-GLUCOSE COTRANSPORTER) - Homo sapiens (Human), 672 aa.	4.20E-53	
314	cg44927952	342	TATTTTTCATTG TACTTATTATTC A[T/C]TATACTTA CTATATATATTT AAAAAC	T	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:AAD34077 CGI- 82 PROTEIN - HOMO SAPIENS (HUMAN), 318 aa.	4.80E-52	
315	cg19885484	77	AAACAACAAAAT AACCAAACATAA A[C/T]CAACTAAT GCTACACAGAAT GTGAT	C	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O15019 KIAA0301 - HOMO SAPIENS (HUMAN), 2047 aa (fragment).	1.90E-51	
316	cg42307356	11	CGGCCGCGGC[G/T]CGGAACGG CGCCTCCCGCC CCACCA	G	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O15121 PUTATIVE FATTY ACID DESATURASE MLD - HOMO SAPIENS (HUMAN), 323 aa.	2.60E-51	
317	cg44005017	947	TGGGAGGCCTG GTTGCCCTCC CGG[C/T]GTGCT GGGACACTCTG GGTTCCTGC	C	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:CAB43363 HYPOTHETICAL 23.0 KD PROTEIN - HOMO SAPIENS (HUMAN), 204 aa.	5.00E-51	
318	cg43329819	609	TTGAGCTCTCCT ACAAAGCTGGAG GC[A/C]AACAGT CAGTGAGAGCG GGGGGGCC	A	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q92565 MYELOBLAST KIAA0277 - HOMO SAPIENS (HUMAN), 580 aa.	1.40E-50	
319	cg43329819	612	AGCTCTCCTACA AGCTGGAGGCA AA[C/T]AGTCAG TGAGAGCGGGG GGGCCAGT	C	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q92565 MYELOBLAST KIAA0277 - HOMO SAPIENS (HUMAN), 580 aa.	1.40E-50	

320	cg43329819	625	GCTGGAGGCAA ACAGTCAGTGA GAG[C/T]GGGG GGCCAGTCAGA CCCGACCAA	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q92565 MYELOBLAST KIAA0277 - HOMO SAPIENS (HUMAN), 580 aa.	1.40E-50	
321	cg44015618	980	CAGCCTCATAG CCACACACACA CAC[A/gap]CGTA CCACACACGCA CACACACACA	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O75148 KIAA0658 PROTEIN - HOMO SAPIENS (HUMAN), 589 aa (fragment).	8.7e-312	11
322	cg44015618	1009	ACCACACACGC ACACACACACA CAC[A/gap]CTTT GTGGCTCAAGT GCAGGCCACA	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O75148 KIAA0658 PROTEIN - HOMO SAPIENS (HUMAN), 589 aa (fragment).	8.7e-312	11
323	cg40361678	3074	CAACACCTTGG GAGGCCGAGGC AGG[T/C]GGATC ACCTGAGGTCA GGAGTTCGA	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW- ACC:P14222 PERFORIN 1 PRECURSOR (P1) (LYMPHOCYTE PORE FORMING PROTEIN) (PFP) (CYTOLYSIN) - Homo sapiens (Human), 555 aa.	9.1e-313	
324	cg40361678	3144	GTGAAACCCCG TCTCTACTAAA AT[AT]CAAAAAT TAGCCGGGCAT GGTGGCG	A	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW- ACC:P14222 PERFORIN 1 PRECURSOR (P1) (LYMPHOCYTE PORE FORMING PROTEIN) (PFP) (CYTOLYSIN) - Homo sapiens (Human), 555 aa.	9.1e-313	
325	cg40361678	3161	CTAAAAATACAA AAATTAGCCGG GC[A/G]TGGTGG CGGATGCCTGT AATCCCAG	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW- ACC:P14222 PERFORIN 1 PRECURSOR (P1) (LYMPHOCYTE PORE FORMING PROTEIN) (PFP) (CYTOLYSIN) - Homo sapiens (Human), 555 aa.	9.1e-313	

326	cg43930957	1287	AAAAATAAACTC TTTTGAAAGTTG T[G/T]GGTCAGC TGACCAGGTAG AGGATTG	G	T	Val	Val	SILENT- CODING	apoptosi s	Human Gene Homologous to SPTREMBL-ID:Q62627 CLONE PAR- 4 INDUCED BY EFFECTORS OF APOPTOSIS - RATTUS NORVEGICUS (RAT), 332 aa.	1.6E-117	
327	cg43300636	413	CAAAGGCGGCA AAGATGGGGAC CAG[C/T]ACCAC AGCGCCACGC CCACCTCCC	C	T	Val	Val	SILENT- CODING	ATPase_ associat ed	Human Gene SPTREMBL-ID:Q29466 VACUOLAR H+-ATPASE SUBUNIT (EC 3.6.1.34) (H(+)-TRANSPORTING ATP SYNTHASE) (H(+)- TRANSPORTING ATPASE) (MITOCHONDRIAL ATPASE) (CHLOROPLAST ATPASE) (COUPLING FACTORS (F(O), F(1) AND CF(1))) - BOS TAURUS (BOVINE), 838 aa.	1.7E-175	
328	cg43967912	749	CATTCTCTCTCC AAAATTTCTCAG AT[C/T]TGTCGA CAGGACTCCATT CCAACC	T	C	Lys	Lys	SILENT- CODING	ATPase_ associat ed	Human Gene Homologous to SPTREMBL-ID:Q22494 SIMILAR TOS. CEREBISIAE VACUOLAR H(+)- ATPASE 54 KD SUBUNIT - CAENORHABDITIS ELEGANS, 470 aa.	5.6E-108	8
329	cg43967912	761	AAAATTTCTCAG ATTTGTGCACAG G[A/G]CTCCATT CCAACCTTCCA GATTAA	A	G	Ser	Ser	SILENT- CODING	ATPase_ associat ed	Human Gene Homologous to SPTREMBL-ID:Q22494 SIMILAR TOS. CEREBISIAE VACUOLAR H(+)- ATPASE 54 KD SUBUNIT - CAENORHABDITIS ELEGANS, 470 aa.	5.60E-108	8
330	cg43967912	773	ATTTGTGCACAG GACTCCATTCCA A[C/T]CTTCCAG ATTTAAGTTCTG AACTGT	C	T	Arg	Arg	SILENT- CODING	ATPase_ associat ed	Human Gene Homologous to SPTREMBL-ID:Q22494 SIMILAR TOS. CEREBISIAE VACUOLAR H(+)- ATPASE 54 KD SUBUNIT - CAENORHABDITIS ELEGANS, 470 aa.	5.60E-108	8
331	cg43132502	371	AGTGGGTGGCA CCGCCGAGGCT GCT[G/A]TTACG GCTCATCTTCAT TGATTTC	G	A	Leu	Leu	SILENT- CODING	ATPase_ associat ed	Human Gene Similar to SPTREMBL- ID:Q15332 GAMMA SUBUNIT OF SODIUM POTASSIUM ATPASE LIKE - HOMO SAPIENS (HUMAN), 126 aa.	9.40E-58	11

337	cg43312829	1422	AGACAACAGGA CTCCATGTAAC GAA/GTATGAG GACAATTGGAAG AAATCAT	A	G	Glu	Glu	SILENT- CODING	dehydrog enase	Human Gene SWISSPROT- ID:Q16134 ELECTRON TRANSFER FLAVOPROTEIN-UBIQUINONE OXIDOREDUCTASE PRECURSOR (EC 1.5.5.1) (ETF-QO) (ETF- UBIQUINONE OXIDOREDUCTASE) (ETF DEHYDROGENASE) (ELECTRON-TRANSFERRING- FLAVOPROTEIN DEHYDROGENASE) - HOMO SAPIENS (HUMAN). 617 aa.	0.00E+00	4
338	cg43312829	1452	AGGACAATTGGA AGAAATCATGG GT[A/G]TGGAAA GAGCTATATTCT GTTAGAA	A	G	Val	Val	SILENT- CODING	dehydrog enase	Human Gene SWISSPROT- ID:Q16134 ELECTRON TRANSFER FLAVOPROTEIN-UBIQUINONE OXIDOREDUCTASE PRECURSOR (EC 1.5.5.1) (ETF-QO) (ETF- UBIQUINONE OXIDOREDUCTASE) (ETF DEHYDROGENASE) (ELECTRON-TRANSFERRING- FLAVOPROTEIN DEHYDROGENASE) - HOMO SAPIENS (HUMAN). 617 aa.	0.00E+00	4
339	cg43312829	1473	GGGTATGGAAA GAGCTATATTCT GTT/CJAGAAATA TAAGGCCATCCT GCCACG	T	C	Val	Val	SILENT- CODING	dehydrog enase	Human Gene SWISSPROT- ID:Q16134 ELECTRON TRANSFER FLAVOPROTEIN-UBIQUINONE OXIDOREDUCTASE PRECURSOR (EC 1.5.5.1) (ETF-QO) (ETF- UBIQUINONE OXIDOREDUCTASE) (ETF DEHYDROGENASE) (ELECTRON-TRANSFERRING- FLAVOPROTEIN DEHYDROGENASE) - HOMO SAPIENS (HUMAN). 617 aa.	0.00E+00	4

340	cg43312829	1569	ACTGGATATTGA GAGGAATGGAG CC[G/A]TGGACT CTAAACATATAA GGCTCTG	G	A	Pro	Pro	SILENT- CODING	dehydrog enase	Human Gene SWISSPROT- ID:Q16134 ELECTRON TRANSFER FLAVOPROTEIN-UBIQUINONE OXIDOREDUCTASE PRECURSOR (EC 1.5.5.1) (ETF-QO) (ETF- UBIQUINONE OXIDOREDUCTASE) (ETF DEHYDROGENASE) (ELECTRON-TRANSFERRING- FLAVOPROTEIN DEHYDROGENASE) - HOMO SAPIENS (HUMAN), 617 aa.	0.00E+00	4
341	cg43312829	1623	TTGAACGGCTC AAGCCAGCCAA GGA[T/C]TGAC ACCCATTGAGTA TCCAAAC	T	C	Asp	Asp	SILENT- CODING	dehydrog enase	Human Gene SWISSPROT- ID:Q16134 ELECTRON TRANSFER FLAVOPROTEIN-UBIQUINONE OXIDOREDUCTASE PRECURSOR (EC 1.5.5.1) (ETF-QO) (ETF- UBIQUINONE OXIDOREDUCTASE) (ETF DEHYDROGENASE) (ELECTRON-TRANSFERRING- FLAVOPROTEIN DEHYDROGENASE) - HOMO SAPIENS (HUMAN), 617 aa.	0.00E+00	4
342	cg43307992	652	TCGAGGGCCCC AACTTTGAGTTC TC[C/A]ACGGAG ACCCATGAGGA GCTGCTGT	C	A	Ser	Ser	SILENT- CODING	dehydrog enase	Human Gene Homologous to SPTREMBL-ID:O00217 MITOCHONDRIAL NADH DEHYDROGENASE-UBIQUINONE FE-S PROTEIN 8, 23 KDA SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 210 aa.	1.70E-113	11
343	cg43369759	965	TGGCTGTGGGC TTCACCAGCCTC AC[C/T]ACCTCC TCCAGGGAGTT GACTTCAG	C	T	Val	Val	SILENT- CODING	dehydrog enase	Human Gene Homologous to SPTREMBL-ID:Q16797 NADP- DEPENDENT MALIC ENZYME (EC 1.1.1.40) (MALATE DEHYDROGENASE (OXALOACETATE DECARBOXYLATING) (NADP+)) (PYRUVIC-MALIC CARBOXYLASE) - HOMO SAPIENS (HUMAN), 572 aa.	1.80E-109	11

344	cg39523614	318	ATGCTGGATCA GATCCAGCTGC ACTATTAAGTGT CGAGCCGACGA AGATGGGG	A	T	Leu	Leu	SILENT- CODING	dehydrog enase	Human Gene Similar to SWISSPROT- ID:P46703 ACYL-COA DEHYDROGENASE (EC 1.3.99.-) - MYCOBACTERIUM LEPRAE, 389 aa.	2.10E-76	
345	cg39523614	360	AAGATGGGGAC AGTTTCGTCCTG AA[C/T]GGCGTC AAGGCTTGGGT CACGGAGG	C	T	Asn	Asn	SILENT- CODING	dehydrog enase	Human Gene Similar to SWISSPROT- ID:P46703 ACYL-COA DEHYDROGENASE (EC 1.3.99.-) - MYCOBACTERIUM LEPRAE, 389 aa.	2.10E-76	
346	cg39523614	366	GGGACAGTTTC GTCCTGAACGG CGT[C/T]AAGGC TTGGGTCACGG AGGCTGGCG	C	T	Val	Val	SILENT- CODING	dehydrog enase	Human Gene Similar to SWISSPROT- ID:P46703 ACYL-COA DEHYDROGENASE (EC 1.3.99.-) - MYCOBACTERIUM LEPRAE, 389 aa.	2.10E-76	
347	cg39523614	613	TCGAGGGCACG GTCTGAGTGT GCTT/CJTGGGT ACGCTTGACAA CTCTCGTGT	T	C	Leu	Leu	SILENT- CODING	dehydrog enase	Human Gene Similar to SWISSPROT- ID:P46703 ACYL-COA DEHYDROGENASE (EC 1.3.99.-) - MYCOBACTERIUM LEPRAE, 389 aa.	2.10E-76	
348	cg39523614	660	GTGTCGATTGG CTGCTCAAGCA GT[G/A]GGAATT GCCCAGGGAGC TTTAGACA	G	A	Val	Val	SILENT- CODING	dehydrog enase	Human Gene Similar to SWISSPROT- ID:P46703 ACYL-COA DEHYDROGENASE (EC 1.3.99.-) - MYCOBACTERIUM LEPRAE, 389 aa.	2.10E-76	
349	cg42717491	207	AGGCTCACACT CACTTCATGTTT TT[C/G]ACAAAG TCCTCGCCTTTC TTGATGG	C	G	Val	Val	SILENT- CODING	dehydrog enase	Human Gene Similar to SWISSPROT- ID:P04636 MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR (EC 1.1.1.37) - RATTUS NORVEGICUS (RAT), 338 aa.	2.40E-52	

350	cg42717491	252	TGATGGAGGCT TTCAGCTCAGG GAT[G/A]GCCTC GGCAATCATTTT CTCCTCAA	G	A	Ala	Ala	SILENT- CODING	dehydrog enase	Human Gene Similar to SWISSPROT- ID:P04636 MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR (EC 1.1.1.37) - RATTUS NORVEGICUS (RAT), 338 aa.	2.40E-52	
351	cg42717491	270	CAGGGATGGCC TCGGCAATCATT TT[C/T]TCCTCAA AAGGAGTGATTT TGCCAA	C	T	Glu	Glu	SILENT- CODING	dehydrog enase	Human Gene Similar to SWISSPROT- ID:P04636 MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR (EC 1.1.1.37) - RATTUS NORVEGICUS (RAT), 338 aa.	2.40E-52	
352	cg42717491	288	TCATTTTCTCCT CAAAAGGAGTG ATT[C/T]TGCCAA TGCTAGGTTCT TCTCCA	T	C	Lys	Lys	SILENT- CODING	dehydrog enase	Human Gene Similar to SWISSPROT- ID:P04636 MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR (EC 1.1.1.37) - RATTUS NORVEGICUS (RAT), 338 aa.	2.40E-52	
353	cg42711596	1535	ATTAGTAGTGCT GTGAGCTGCTTT TT[G/G]TTGAATC TGATTTAGTTTC AGTTC	T	G	Thr	Thr	SILENT- CODING	eph	Human Gene Homologous to SWISSPROT-ID:P48722 OSMOTIC STRESS PROTEIN 94 (HEAT SHOCK 70-RELATED PROTEIN APG- 1) - MUS MUSCULUS (MOUSE), 838 aa.	2.10E-115	4
354	cg43319420	1557	AGAAAGTCAGAA GGCCTTCCTGT GGC[A/C]CCGTT CATGGACCGAG ACAAAGTGA	A	C	Ala	Ala	SILENT- CODING	esterase	Human Gene Similar to SWISSNEW- ID:Q23917 3',5'-CYCLIC- NUCLEOTIDE PHOSPHODIESTERASE REGA (EC 3.1.4.17) (PDEASE REGA) - DICTYOSTELIUM DISCOIDEUM (SLIME MOLD), 793 aa. pcls: SWISSPROT-ID:Q23917 3',5'- CYCLIC-NUCLEOTIDE PHOSPHODIESTERASE REGA (EC 3.1.4.17) (PDEASE REGA) - DICTYOSTELIUM DISCOIDEUM (SLIME MOLD), 793.aa.	3.30E-60	21

355	cg41029366	687	AGTGGGGATCA GTGTGCGATGA CACT/CJTGGGA CCTGGAGGACG CCCACGTGG	T	C	Thr	SILENT- CODING	glycoprotein	Human Gene SPTREMBL-ID:Q61003 T CELL SURFACE GLYCOPROTEIN CD6 - MUS MUSCULUS (MOUSE), 665 aa.	1.00E-234	11
356	cg42876034	860	GCGCCCGCCGC GGCAGCGCCCC GAG[G/C]CCGGC TTCGGCCCCGA GCCTGGACG	G	C	Gly	SILENT- CODING	glycoprotein	Human Gene Similar to SWISSPROT- ID:Q07066 22 KD PEROXISOMAL MEMBRANE PROTEIN - RATTUS NORVEGICUS (RAT), 193 aa.	2.60E-78	
357	cg43976227	258	CTGGTGTGATCT CTGTCTCTTTAT G[G/A]ACCACTA CTTTGGTCACTG ACATGT	G	A	Val	SILENT- CODING	glycoprotein	Human Gene Similar to SPTREMBL- ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa.	2.60E-60	18
358	cg43916642	816	GGCTGAAAAGC ATATCTATACAT TC[G/A]GAGAAG TCGCAAATAGAA AGGAAAA	G	A	Ser	SILENT- CODING	helicase	Human Gene Similar to SWISSPROT- ID:P25888 PUTATIVE ATP- DEPENDENT RNA HELICASE RHLE ESCHERICHIA COLI, 454 aa.	2.90E-54	1
359	cg43925670	2320	AACCAGCATCA CCTCGGAACCTT TC[T/C]TCCATCA AGTCAGCAATCT GAATTT	T	C	Glu	SILENT- CODING	interferon	Human Gene SWISSPROT- ID:Q16666 GAMMA-INTERFERON- INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa. ipclis:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment).	0.00E+00	1

360	cg43925670	2370	TTGTCATACTCT TCTCTCATTTTT A[A/G]ATTAAAGTT TTAAATCGTTGC TCAGT	A	G	Leu	Leu	SILENT- CODING	interferon	Human Gene SWISSPROT- ID:Q16666 GAMMA-INTERFERON- INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa.lpcis:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment)	0.00E+00	1
361	cg43925670	2389	TTTTTAAATTAA GTTTAAATCGT T[G/A]CTCAGTA AGGACTTAACCA TTCTAA	G	A	Ser	Ser	SILENT- CODING	interferon	Human Gene SWISSPROT- ID:Q16666 GAMMA-INTERFERON- INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa.lpcis:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment)	0.00E+00	1
362	cg43925670	2446	AATCATTGATGA CCTCTAATCCTT TT[C/j]AGTAGAA CAATGTTCTTGT ATTTTT	T	C	Leu	Leu	SILENT- CODING	interferon	Human Gene SWISSPROT- ID:Q16666 GAMMA-INTERFERON- INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa.lpcis:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment)	0.00E+00	1

363	cg44004587	1913	TTTTATTGTCAT TTTCATCAATAA GIG/AJATACACA TCTCTGCCAGG AGTTGAA	G	A	Ile	Ile	SILENT- CODING	isomerase	Human Gene Homologous to SPTREMBL-ID:Q13907 HOMOLOG OF YEAST IPP ISOMERASE - HOMO SAPIENS (HUMAN), 228 aa.	3.00E-123	
364	cg43257400	2144	CATGTGTGGTAA CTCCTCAAGATG GIG/CJGAGACGT TAGCACAAATGA TAGAAG	G	C	Gly	Gly	SILENT- CODING	kinase	Human Gene SPTREMBL-ID:Q60680 CONSERVED HELIX-LOOP-HELIX UBIQUITOUS KINASE - MUS MUSCULUS (MOUSE), 745 aa.	0.00E+00	10
365	cg43931272	2072	TTGGTGGTCTT TCCCAACCAACAA A[A/G]CACTCCG GTGGTAAATACC AATAAG	A	G	Cys	Cys	SILENT- CODING	kinase	Human Gene TREMBLNEW- ID:G2853031 TOUSLED-LIKE KINASE - MUS MUSCULUS (MOUSE), 717 aa.	0.00E+00	
366	cg42665067	748	GGGGCTTCTAC ATATCCCCCG AAG[C/T]ACCTT CAGCACTCTGC AGGAGCTGG	C	T	Ser	Ser	SILENT- CODING	kinase	Human Gene SWISSPROT- ID:P08631 TYROSINE-PROTEIN KINASE HCK (EC 2.7.1.12) (P59- HCK AND P60-HCK) (HEMOPOIETIC CELL KINASE) - HOMO SAPIENS (HUMAN), 526 aa.	9.20E-289	20 (20q11)
367	cg43982923	634	CGATGCAGAAA TACGAGAAACT GGA[A/G]AAGAT TGGGGAAGGCA CCTACGGAA	A	G	Glu	Glu	SILENT- CODING	kinase	Human Gene SWISSPROT- ID:P49615 CELL DIVISION PROTEIN KINASE 5 (EC 2.7.1.-) (TAU PROTEIN KINASE II CATALYTIC SUBUNIT) (TPKII CATALYTIC SUBUNIT) (KINASE PSSALRE) (CRK6) - MUS MUSCULUS (MOUSE), 292 aa.	3.60E-159	19
368	cg43982923	655	TGGAAGAAGATTG GGGAAGGCACC TA[C/T]GGAAC GTGTTCAAGGC CAAAAACC	C	T	Tyr	Tyr	SILENT- CODING	kinase	Human Gene SWISSPROT- ID:P49615 CELL DIVISION PROTEIN KINASE 5 (EC 2.7.1.-) (TAU PROTEIN KINASE II CATALYTIC SUBUNIT) (TPKII CATALYTIC SUBUNIT) (KINASE PSSALRE) (CRK6) - MUS MUSCULUS (MOUSE), 292 aa.	3.60E-159	19

369	cg43982923	697	CCAAAAACCGG GAGACTCATGA GATC/TGTGGC TCTGAAACGGG TGAGGCTGG	C	T	Ile	Ile	SILENT- CODING	kinase	Human Gene SWISSPROT- ID:P49615 CELL DIVISION PROTEIN KINASE 5 (EC 2.7.1.-) (TAU PROTEIN KINASE II CATALYTIC SUBUNIT) (TPKII CATALYTIC SUBUNIT) (KINASE PSSALRE) (CRK6) - MUS MUSCULUS (MOUSE), 292 aa.	3.60E-159	19
370	cg43919086	576	CGCTCAGGAGG ATATAGGTGATG AC/A/GJCCGATG CTCCACATGTCC GCCTCCA	A	G	Gly	Gly	SILENT- CODING	kinase	Human Gene TREMBLNEW- ID:D1025880 ZIP-KINASE - HOMO SAPIENS (HUMAN), 454 aa.	6.80E-158	19
371	cg25143358	407	GGCGGGCTTCA AGTTTCGTGGTC AT/G/AJCCGCCG GTTCCCAACCCC CGAACCAG	G	A	Gly	Gly	SILENT- CODING	kinase	Human Gene Similar to SWISSPROT- ID:P46546 GLUTAMATE 5-KINASE (EC 2.7.2.11) (GAMMA-GLUTAMYL KINASE) (GK) - CORYNEBACTERIUM GLUTAMICUM, 369 aa.	2.70E-51	
372	cg43105476	514	GGTCCGATGC CCCACATTGCT GGC/C/TJGTGTG CTTCACCAGGA ACTCCACCA	C	T	Thr	Thr	SILENT- CODING	kinasein hibitor	Human Gene Similar to SWISSPROT- ID:P42773 CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) - HOMO SAPIENS (HUMAN), 168 aa.	7.80E-86	
373	cg43105476	541	TGTGCTTCACCA GGAACCTCCACC AC/C/AJCGGAGG TGGCCTTCTTTG GCAGCCA	C	A	Arg	Arg	SILENT- CODING	kinasein hibitor	Human Gene Similar to SWISSPROT- ID:P42773 CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) - HOMO SAPIENS (HUMAN), 168 aa.	7.80E-86	
374	cg43105476	595	GCAAGGGCAGG TTCCCTTCATTA TC/C/TJCGATGT TAACATCAGCTT GAAACT	C	T	Glu	Glu	SILENT- CODING	kinasein hibitor	Human Gene Similar to SWISSPROT- ID:P42773 CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) - HOMO SAPIENS (HUMAN), 168 aa.	7.80E-86	

375	cg43105476	616	TATCCTCGATGT TAACATCAGCTT G/A/GAACTCCA GCAAAGTCTGTA AAGTGT	A	G	Phe	Phe	SILENT- CODING	kinasere hibitor	Human Gene Similar to SWISSPROT- ID:P42773 CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) - HOMO SAPIENS (HUMAN), 168 aa.	7.80E-86	
376	cg43939695	410	CAGGGAACAGC AATGGGAACGC CAGT/CJATCAA CATCACGGACA TCTCAAGGA	T	C	Ser	Ser	SILENT- CODING	kinasere ceptor	Human Gene SWISSPROT- ID:Q16288 NT-3 GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (TRKC TYROSINE KINASE) (GP145-TRKC) (TRK-C) - HOMO SAPIENS (HUMAN), 839 aa.	0.00E+00	15 (15q25)
377	cg43939695	419	GCAATGGGAAC GCCAGTATCAA CAT/C/JACGGA CATCTCAAGGAA TATCACTT	C	T	Ile	Ile	SILENT- CODING	kinasere ceptor	Human Gene SWISSPROT- ID:Q16288 NT-3 GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (TRKC TYROSINE KINASE) (GP145-TRKC) (TRK-C) - HOMO SAPIENS (HUMAN), 839 aa.	0.00E+00	15 (15q25)
378	cg43939695	467	CTTCCATACACA TAGAGAACTGG CG/C/AJAGTCTT CACACGCTCAA CGCCGTGG	C	A	Arg	Arg	SILENT- CODING	kinasere ceptor	Human Gene SWISSPROT- ID:Q16288 NT-3 GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (TRKC TYROSINE KINASE) (GP145-TRKC) (TRK-C) - HOMO SAPIENS (HUMAN), 839 aa.	0.00E+00	15 (15q25)
379	cg43939695	473	TACACATAGAGA ACTGGCGCAGT CTT/G/CACACG CTCAACGCCGT GGACATGG	T	G	Leu	Leu	SILENT- CODING	kinasere ceptor	Human Gene SWISSPROT- ID:Q16288 NT-3 GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (TRKC TYROSINE KINASE) (GP145-TRKC) (TRK-C) - HOMO SAPIENS (HUMAN), 839 aa.	0.00E+00	15 (15q25)
380	cg43939695	479	TAGAGAACTGG CGCAGTCTTCA CAC/G/AJCTCAA CGCCGTGGACA TGGAGCTCT	G	A	Thr	Thr	SILENT- CODING	kinasere ceptor	Human Gene SWISSPROT- ID:Q16288 NT-3 GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (TRKC TYROSINE KINASE) (GP145-TRKC) (TRK-C) - HOMO SAPIENS (HUMAN), 839 aa.	0.00E+00	15 (15q25)

381	cg43939695	485	ACTGGCGCAGT C CTTCACACGCTC AA[C/T]GCCGTG GACATGGAGCT CTACACCG	C	T	Asn	Asn	SILENT- CODING	kinasere ceptor	Human Gene SWISSPROT- ID:Q16288 NT-3 GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (TRKC TYROSINE KINASE) (GP145-TRKC) (TRK-C) - HOMO SAPIENS (HUMAN), 839 aa.	0.00E+00	15 (15q25)
382	cg43939695	509	ACGCCGTGGAC ATGGAGCTCTA CAC[C/G]GGACT TCAAAAGCTGAC CATCAAGA	C	G	Thr	Thr	SILENT- CODING	kinasere ceptor	Human Gene SWISSPROT- ID:Q16288 NT-3 GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (TRKC TYROSINE KINASE) (GP145-TRKC) (TRK-C) - HOMO SAPIENS (HUMAN), 839 aa.	0.00E+00	15 (15q25)
383	cg43939695	518	ACATGGAGCTC A TACACCGGACTT CA[A/G]AAGCTG ACCATCAAGAAC TCAGGAC	A	G	Gln	Gln	SILENT- CODING	kinasere ceptor	Human Gene SWISSPROT- ID:Q16288 NT-3 GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (TRKC TYROSINE KINASE) (GP145-TRKC) (TRK-C) - HOMO SAPIENS (HUMAN), 839 aa.	0.00E+00	15 (15q25)
384	cg29023997	183	TGGTTCCATT G TCAATCTGGATG G[G/A]ATGGAGC ACCATGTGCGC ACCTGCA	G	A	Gly	Gly	SILENT- CODING	kinasere ceptor	Human Gene SWISSPROT- ID:P36896 SERINE/THREONINE- PROTEIN KINASE RECEPTOR R2 PRECURSOR (EC 2.7.1.37) (SKR2) (ACTIVIN RECEPTOR-LIKE KINASE 4) (ALK-4) (ACTR-IB) - HOMO SAPIENS (HUMAN), 505 aa.	9.30E-280	12
385	cg43942537	2040	GTTCTTCTAGGG T CCTGTAAACCTT CT[C/T]TTCACCTC TTCTTTAGAGGC ATCAT	T	C	Lys	Lys	SILENT- CODING	kinesin	Human Gene SWISSNEW-ID:P33176 KINESIN HEAVY CHAIN (UBIQUITOUS KINESIN HEAVY CHAIN) (UKHC) - HOMO SAPIENS (HUMAN), 963 aa. pcls: SWISSPROT- ID:P33176 KINESIN HEAVY CHAIN (UBIQUITOUS KINESIN HEAVY CHAIN) (UKHC) - HOMO SAPIENS (HUMAN), 963 aa.	0.00E+00	10
386	cg43975720	2368	TCCGGAAGTGG C AAGTGGTACCA GTT[C/T]ACGTCT CTGCGGGACCT GCTGTGGG	C	T	Phe	Phe	SILENT- CODING	kinesin	Human Gene SWISSPROT- ID:Q12756 KINESIN-LIKE PROTEIN KIF1A (AXONAL TRANSPORTER OF SYNAPTIC VESICLES) - HOMO SAPIENS (HUMAN), 1690 aa.	0.00E+00	2

387	cg43975720	2398	CTCTGCGGGAC CTGCTGTGGGG CAA[C/T]GCCAT CTTCCTCAAGGA GGCCAATG	C	T	Asn	Asn	SILENT- CODING	kinesin	Human Gene SWISSPROT- ID:Q12756 KINESIN-LIKE PROTEIN KIF1A (AXONAL TRANSPORTER OF SYNAPTIC VESICLES) - HOMO SAPIENS (HUMAN), 1690 aa.	0.00E+00	2
388	cg43311943	44	TCGGGCCCGAT GACCCCAATGT GGC[G/C]AAGAC CAAGAACAACCT GGCTTCCT	G	C	Ala	Ala	SILENT- CODING	kinesin	Human Gene Similar to SWISSPROT- ID:Q05090 KINESIN LIGHT CHAIN (KLC) - STRONGYLOCENTROTUS PURPURATUS (PURPLE SEA URCHIN), 686 aa.	8.80E-51	
389	cg43311943	80	ACAACCTGGCTT CCTGCTACCTG AA[A/G]CAGGGC AAGTACCAGGA TGCAGAGA	A	G	Lys	Lys	SILENT- CODING	kinesin	Human Gene Similar to SWISSPROT- ID:Q05090 KINESIN LIGHT CHAIN (KLC) - STRONGYLOCENTROTUS PURPURATUS (PURPLE SEA URCHIN), 686 aa.	8.80E-51	
390	cg43983535	4764	TCTCTGGGGCC CGCTGAGGTGA CAG[C/T]AAGTG CTTAGCTCCTG AGTCATAT	C	T	Leu	Leu	SILENT- CODING	laminin	Human Gene SWISSPROT- ID:P24043 LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN) - HOMO SAPIENS (HUMAN), 3110 aa.	0.00E+00	6 (6q22)
391	cg42488873	304	ATCCTTTGAAAA TCTCATATTGTT T[C/T]GAGTTTTC ATTACTTCCATA CAAAG	C	T	Ser	Ser	SILENT- CODING	lipase	Human Gene SWISSPROT- ID:P54317 PANCREATIC LIPASE RELATED PROTEIN 2 PRECURSOR (EC 3.1.1.3) - HOMO SAPIENS (HUMAN), 469 aa.	9.80E-261	
392	cg43935885	3848	GGAAGCCCCAG CTGCAGGAGCT GCT[A/G]AAGCT GCCCGCCTTCA TGCGGGTAA	A	G	Leu	Leu	SILENT- CODING	MHC	Human Gene SPTREMBL-ID:P79457 MALE-SPECIFIC HISTOCOMPATIBILITY ANTIGEN H- YDB - MUS MUSCULUS (MOUSE), 1186 aa.	7.20E-173	
393	cg44019843	955	ATGTGGAGTAC ACCTTCACAGG GAT[C/T]TACAC CTTTGAGTCCCT CATCAAGA	C	T	Ile	Ile	SILENT- CODING	misc_ch annel	Human Gene SPTREMBL-ID:Q15478 SODIUM CHANNEL ALPHA SUBUNIT - HOMO SAPIENS (HUMAN), 1836 aa.	0.00E+00	17 (17q23.1)

394	cg44929972	1266	ATGTCCTGAGG GCAGTGGAGGA ACG[G/A]GATTT TCCAACAGAAAC CATTAAAT	G	A	Arg	Arg	SILENT- CODING	ngf	Human Gene TREMBLNEW- ID:E1216872 NERVE GROWTH FACTOR-INDUCIBLE PC4 HOMOLOGUE - HOMO SAPIENS (HUMAN), 453 aa. Human Gene SWISSPROT- ID:Q01831 DNA-REPAIR PROTEIN COMPLEMENTING XP-C CELLS (XERODERMA PIGMENTOSUM GROUP C COMPLEMENTING PROTEIN) (P125) - HOMO SAPIENS (HUMAN), 939 aa.	4.70E-214	7
395	cg44926604	1283	AGTCGATGTCC AGCTTGCGGGC CAC[G/A]CGGTG TAGATTGGGCA GGTTCAGCT	G	A	Arg	Arg	SILENT- CODING	nuclease	ID:Q01831 DNA-REPAIR PROTEIN COMPLEMENTING XP-C CELLS (XERODERMA PIGMENTOSUM GROUP C COMPLEMENTING PROTEIN) (P125) - HOMO SAPIENS (HUMAN), 939 aa.	0.00E+00	3
396	cg38642684	282	GCCAGTTAATAT TGCCTAGTAATT T[C/T]TGATAATC ATTAAAGGTATG TAAGT	C	T	Gln	Gln	SILENT- CODING	nuclease	Human Gene Similar to SWISSNEW- ID:P10266 RETROVIRUS-RELATED POL POLYPOLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] - HOMO SAPIENS (HUMAN), 874 aa.lpcds:SWISSPROT-ID:P10266 RETROVIRUS-RELATED POL POLYPOLYPROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) - HOMO SAPIENS (HUMAN), 874 aa.	2.60E-50	
397	cg38642684	387	AAGGATACCTTCC AAGGAGAGGAC ATT[C/T]GTACTT TTTCAGGTGCAA TGATTA	T	C	Gln	Gln	SILENT- CODING	nuclease	Human Gene Similar to SWISSNEW- ID:P10266 RETROVIRUS-RELATED POL POLYPOLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] - HOMO SAPIENS (HUMAN), 874 aa.lpcds:SWISSPROT-ID:P10266 RETROVIRUS-RELATED POL POLYPOLYPROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) - HOMO SAPIENS (HUMAN), 874 aa.	2.60E-50	

398	cg38642684	405	AGGACATTGTGTA CTTTTCAGGTG C[A/T]ATGATTAA ACCACTTAACTG TGCA T	A	T	Ile	Ile	SILENT- CODING	nuclease	Human Gene Similar to SWISSNEW- ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] - HOMO SAPIENS (HUMAN), 874 aa. pcis:SWISSPROT-ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49)); ENDONUCLEASE) - HOMO SAPIENS (HUMAN), 874 aa.	2.60E-50	
399	cg38642684	456	TCCTTATGACAG AGGTATATAAAC TT[C]AAAAAGCA CTGGCTCCACT GGGGCTG	T	C	Leu	Leu	SILENT- CODING	nuclease	Human Gene Similar to SWISSNEW- ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] - HOMO SAPIENS (HUMAN), 874 aa. pcis:SWISSPROT-ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49)); ENDONUCLEASE) - HOMO SAPIENS (HUMAN), 874 aa.	2.60E-50	
400	cg43919677	2577	TGAAGTAGCTC CTGAAGCTTCTA C[G/A]TCTAGTG CCAGCCAAGTG ATTGCTC	G	A	Thr	Thr	SILENT- CODING	oncogen e	Human Gene SWISSPROT- ID:Q00918 LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR (TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1- BP- 1) (TRANSFORMING GROWTH FACTOR BETA-1 MASKING PROTEIN, LARGE SUBUNIT) - RATTUS NORVEGICUS (RAT), 1712 aa.	0.00E+00	2 (2p12)

401	cg44005163	1384	CCTGTGGGCTG ATTACATTAACT GAT/CIGCACAA AGATTATGTAAT GCTTTAT	T	C	Asp	Asp	SILENT- CODING	oncogene	Human Gene SWISSPROT- ID:P12756 SKI-RELATED ONCOGENE SNOA - HOMO SAPIENS (HUMAN), 415 aa.	5.30E-229	
402	cg44005163	1423	GTAATGCTTTAT TGCGGCCACGA ACT/GJTTCCTC AAATGGTAGC GTACTTC	T	G	Thr	Thr	SILENT- CODING	oncogene	Human Gene SWISSPROT- ID:P12756 SKI-RELATED ONCOGENE SNOA - HOMO SAPIENS (HUMAN), 415 aa.	5.30E-229	
403	cg25334466	546	TCAAGGACCAG TTCACCTACCCTC CC/T/CJGAGGTG AAGGACTGATG CTTTGCCA	T	C	Pro	Pro	SILENT- CODING	oxidase	Human Gene Homologous to SWISSPROT-ID:P25689 URICASE (EC 1.7.3.3) (URATE OXIDASE) - PAPIO HAMADRYAS (HAMADRYAS BABOON), 303 aa.	1.30E-149	
404	cg42535091	750	AACTGAAATACG ACGTTGGTGA GG/G/GGAACGG TTTGATCTTTG ACAGATC	A	G	Gly	Gly	SILENT- CODING	phosphatase	Human Gene SWISSPROT- ID:Q06124 PROTEIN-TYROSINE PHOSPHATASE 2C (EC 3.1.3.48) (PTP-2C) (PTP-1D) (SH-PTP3) (SH- PTP2) - HOMO SAPIENS (HUMAN), 593 aa.	0.00E+00	12
405	cg43302847	1227	GGTGGTGGTGG CCATCCAGATC CTG/C/AJGGAAG AACCCCAAAGG CTTCTTCTT	C	A	Arg	Arg	SILENT- CODING	phosphatase	Human Gene SWISSPROT- ID:P05186 ALKALINE PHOSPHATASE, TISSUE- NONSPECIFIC ISOZYME PRECURSOR (EC 3.1.3.1) (AP- TNAP) (LIVER/BONE/KIDNEY ISOZYME) (TNSALP) - HOMO SAPIENS (HUMAN), 524 aa.	3.20E-286	1 (1p36.1)
406	cg39728924	433	GGCAAAATGGTG TTGGAAAAATAAT TC/G/AJAATGTTA TTGCCATGATAA CCAGAG	G	A	Ser	Ser	SILENT- CODING	phosphatase	Human Gene Similar to TREMBLNEW-ID:D1024666 PROTEIN-TYROSINE- PHOSPHATASE (EC 3.1.3.48) - MUS MUSCULUS (MOUSE), 426 aa.	1.20E-64	

407	cg42881873	1564	ACCTGAAAGCG AGCGACTGGAA AGT[A/G]AACGG CGCGGGTCATA AAGTTAGCC	A	G	Val	Val	SILENT- CODING	protease	Human Gene SWISSNEW-ID:P29122 SUBTILISIN-LIKE PROTEASE PACE4 PRECURSOR (EC 3.4.21.-) - HOMO SAPIENS (HUMAN), 969 aa.lpcis:SWISSPROT-ID:P29122 SUBTILISIN-LIKE PROTEASE PACE4 PRECURSOR (EC 3.4.21.-) - HOMO SAPIENS (HUMAN), 969 aa.	0.00E+00	15 (15q26)
408	cg42913398	589	CTGTTCCGTGG ATGAGAAGATA GTC[T/C]ACATTT CTGAAATATTCT GCCTCTG	T	C	Val	Val	SILENT- CODING	protease	Human Gene SPTREMBL-ID:O00199 INTEGRAL MEMBRANE SERINE PROTEASE SEPRASE - HOMO SAPIENS (HUMAN), 760 aa.	0.00E+00	2
409	cg44028327	793	TTCGAATTACCT ACTCAATTGTGC A[A/G]ACGAATT GTTCCAAAGAG AATTTTC	A	G	Gln	Gln	SILENT- CODING	protease nhib	Human Gene SWISSPROT- ID:P01042 KININOGEN, HMW PRECURSOR (ALPHA-2-THIOL PROTEINASE INHIBITOR) (CONTAINS: BRADYKININ) - HOMO SAPIENS (HUMAN), 644 aa.	0.00E+00	3 (3q27)
410	cg43979831	899	CCTCAAGGACC ACTCCCAAAGA CTT[C/T]TATGTT GATGAGAACAC AACAGTCC	C	T	Phe	Phe	SILENT- CODING	protease nhib	Human Gene SWISSPROT- ID:P29622 KALLISTATIN PRECURSOR (KALLIKREIN INHIBITOR) (PROTEASE INHIBITOR 4) - HOMO SAPIENS (HUMAN), 427 aa.	1.10E-228	14
411	cg43987538	905	ATCATCATAAGA GAAGAATCATTT TTT[A/CC]AGTAG CCCCACTACCAT GAATGA	T	A	Gly	Gly	SILENT- CODING	reductas e	Human Gene SWISSPROT- ID:Q08257 QUINONE OXIDOREDUCTASE (EC 1.6.5.5) (NADPH:QUINONE REDUCTASE) (ZETA- CRYSTALLIN) - HOMO SAPIENS (HUMAN), 329 aa.	1.10E-171	1 (1p31)
412	cg42717608	142	CCCACAAAGTC TATGTCCAGCAC CT[G/T]CTGAAG AGAGACAAAGA ACACCTGT	G	T	Leu	Leu	SILENT- CODING	reductas e	Human Gene Similar to SWISSNEW- ID:P37040 NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR) - MUS MUSCULUS (MOUSE), 677 aa.lpcis:SWISSPROT-ID:P37040 NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR) - MUS MUSCULUS (MOUSE), 677 aa.	1.80E-51	

413	cg43927378	4726	ATCTGATGGAG AACTACCAGATC GTT/CJGTACG AACCTGGCCAC	T	C	Val	Val	SILENT- CODING	struct	Human Gene SPTREMBL-ID:Q13459 MYOSIN-IXB - HOMO SAPIENS (HUMAN), 2022 aa.	0	2
414	cg43945592	1503	TGAGCGTG GGGCTCGGCA GGGTACACAAA CTC[T/C]GTGGC TGCAAAATCCCC AGAGGAGC	T	C	Thr	Thr	SILENT- CODING	struct	Human Gene TREMBLNEW- ID:G2961252 SUPERVILLIN - HOMO SAPIENS (HUMAN), 1788 aa.	0	10
415	cg43957486	1475	CTGGGGCTCCC CGCTGCCAGTG CCC[A/G]GCCGG CGCCGCCCTGC AGGCAGACG	A	G	Pro	Pro	SILENT- CODING	struct	Human Gene SWISSPROT- ID:P07204 THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM) (CD141 ANTIGEN) - HOMO SAPIENS (HUMAN), 575 aa.	0.00E+00	20 (20p11.2)
416	cg44932934	815	TGCTCGAGGAT GTCAACCGCAT GTC[G/A]CCTGG GGCGCTGCCCA TTATCTTCG	G	A	Ser	Ser	SILENT- CODING	struct	Human Gene SPTREMBL-ID:Q63358 MYOSIN HEAVY CHAIN - RATTUS NORVEGICUS (RAT), 1980 aa.	2.10E-179	
417	cg43100187	320	AACGCCCTAGAG GGGAGCTGGT GGC[C/A]CATGA GCCTGCCATCC AGAATGTGC	C	A	Ala	Ala	SILENT- CODING	struct	Human Gene SWISSPROT- ID:P02549 SPECTRIN ALPHA CHAIN, ERYTHROCYTE - HOMO SAPIENS (HUMAN), 2418 aa.	1.80E-169	
418	cg42930605	333	GGTCCATGCAC ACCTTGCTTC GA[G/A]CCCAGC AGGCCCTTGAG CATGGCAT	G	A	Gly	Gly	SILENT- CODING	struct	Human Gene Similar to SWISSPROT- ID:P48788 TROPONIN I, FAST SKELETAL MUSCLE (TROPONIN I, FAST-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 181 aa.	1E-92	11 (11p15.5)
419	cg42930605	411	GGGGCCGCTTG AACTTGCCCCG CAG[A/G]TCAAA TAGCTTCTGGTT CATGTCCT	A	G	Asp	Asp	SILENT- CODING	struct	Human Gene Similar to SWISSPROT- ID:P48788 TROPONIN I, FAST SKELETAL MUSCLE (TROPONIN I, FAST-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 181 aa.	1E-92	11 (11p15.5)

420	cg42930605	435	GATCAAATAGCT C TCTGGTTCATGT C[C/T]TCCAGCT CCTTGCTGGTCT TCTGCA	T	Glu	Glu	SILENT- CODING	struct	Human Gene Similar to SWISSPROT- ID:P48788 TROPONIN I, FAST SKELETAL MUSCLE (TROPONIN I, FAST-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 181 aa.	1E-92	11 (11p15.5)
421	cg42930605	477	TCTCTGCACCC G TCACCTCCATGT C[G/A]TACTTCTC CTCTTCAGCCG CATCGA	A	Tyr	Tyr	SILENT- CODING	struct	Human Gene Similar to SWISSPROT- ID:P48788 TROPONIN I, FAST SKELETAL MUSCLE (TROPONIN I, FAST-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 181 aa.	1E-92	11 (11p15.5)
422	cg42930605	507	TCTCCTCTTCAG G CCGCATCGATC TT[G/C]GCGTGC AGCTGTTTGCA	C	Ala	Ala	SILENT- CODING	struct	Human Gene Similar to SWISSPROT- ID:P48788 TROPONIN I, FAST SKELETAL MUSCLE (TROPONIN I, FAST-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 181 aa.	1E-92	11 (11p15.5)
423	cg42930605	516	GAGCTCCT C CAGCCGCATCG ATCTTGCGGTG CAG[C/T]TGTT GCAGAGCTCCT	T	Gln	Gln	SILENT- CODING	struct	Human Gene Similar to SWISSPROT- ID:P48788 TROPONIN I, FAST SKELETAL MUSCLE (TROPONIN I, FAST-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 181 aa.	1E-92	11 (11p15.5)
424	cg42930605	528	TCTTGGCGTGC C AGCTGTTTGCA GAG[C/T]TCTG CACTTCAGACAT GGAGCCCG	T	Glu	Glu	SILENT- CODING	struct	Human Gene Similar to SWISSPROT- ID:P48788 TROPONIN I, FAST SKELETAL MUSCLE (TROPONIN I, FAST-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 181 aa.	1E-92	11 (11p15.5)
425	cg42930605	558	GCACTTCAGAC A ATGGAGCCCGG GAT[A/G]TGCAG CGGCGGGCAGT GCTCCGCCA	G	His	His	SILENT- CODING	struct	Human Gene Similar to SWISSPROT- ID:P48788 TROPONIN I, FAST SKELETAL MUSCLE (TROPONIN I, FAST-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 181 aa.	1E-92	11 (11p15.5)
426	cg42930605	564	CAGACATGGAG C CCCGGGATATG CAG[C/A]GGCGG GCAGTGCTCCG CCAGGTAGT	A	Pro	Pro	SILENT- CODING	struct	Human Gene Similar to SWISSPROT- ID:P48788 TROPONIN I, FAST SKELETAL MUSCLE (TROPONIN I, FAST-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 181 aa.	1E-92	11 (11p15.5)

427	cg42930605	615	TCTGCTTCTCTG CCTCAGGCGG CTC/TTCCTCCT TCTCCAGCTCC GTGGCCG	C	T	Glu	Glu	SILENT- CODING	struct	Human Gene Similar to SWISSPROT- ID:P48788 TROPONIN I, FAST SKELETAL MUSCLE (TROPONIN I, FAST-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 181 aa.	1E-92	11 (11p15.5)
428	cg42930605	621	TCTCTGCCTCAC GGCGGCTCTCC TCIC/TJTTCTCCA GCTCCGTGGCC GCTATCT	C	T	Lys	Lys	SILENT- CODING	struct	Human Gene Similar to SWISSPROT- ID:P48788 TROPONIN I, FAST SKELETAL MUSCLE (TROPONIN I, FAST-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 181 aa.	1E-92	11 (11p15.5)
429	cg42893961	51	AATGGCCAGCA GGAAGCGGGG ACC[C/A]GGGGC AAGGTGGCAGC CACCAAGCA	C	A	Arg	Arg	SILENT- CODING	struct	Human Gene Similar to SPTREMBL- ID:Q01449 MYOSIN REGULATORY LIGHT CHAIN, CARDIAC MUSCLE ISOFORM - HOMO SAPIENS (HUMAN), 175 aa.	2.5E-89	
430	cg42475816	282	AATCAAGACAAA CCCGAATTGAAA A[G/A]AAGATTG AAGCCCACTTTG ATGCCA	G	A	Lys	Lys	SILENT- CODING	struct	Human Gene Similar to SPTREMBL- ID:Q10466 TITIN, HEART ISOFORM N2-B (EC 2.7.1.-) (CONNECTIN) - HOMO SAPIENS (HUMAN), 26926 aa.	7.3E-85	2 (2q24.3)
431	cg42522566	337	TGAAGAACGTAA AGGACCGGAG GAT/CJGTGAAG AATGAGGTCAA CATCATGA	T	C	Asp	Asp	SILENT- CODING	struct	Human Gene Similar to SWISSPROT- ID:P07313 MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (EC 2.7.1.117) (MLCK) - ORYCTOLAGUS CUNICULUS (RABBIT), 607 aa.	6E-55	

432	cg43297806	953	GTAGATGGGTA GAATAGTAGCC AGG[G/A]ACAAG ACAGCGGTTCT GCAGGGAGC	A	Val	SILENT- CODING	sulfotran sferase	Human Gene SWISSPROT- ID:P52849 HEPARIN SULFATE N- DEACETYLASE/N- SULFOTRANSFERASE (EC 2.8.2.-) (N- HSST) (N-HEPARIN SULFATE SULFOTRANSFERASE) (GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE) - HOMO SAPIENS (HUMAN), 883 aa.lpcis:TREMBLNEW-ID:G2792518 HEPARAN GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE-2 - HOMO SAPIENS (HUMAN), 883.aa	0.00E+00	10
433	cg43297806	962	TAGAATAGTAGC CAGGGACAAGA CA[G/A]CGGTTT TGCAGGGAGCG TAGTGCCA	A	Arg	SILENT- CODING	sulfotran sferase	Human Gene SWISSPROT- ID:P52849 HEPARIN SULFATE N- DEACETYLASE/N- SULFOTRANSFERASE (EC 2.8.2.-) (N- HSST) (N-HEPARIN SULFATE SULFOTRANSFERASE) (GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE) - HOMO SAPIENS (HUMAN), 883 aa.lpcis:TREMBLNEW-ID:G2792518 HEPARAN GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE-2 - HOMO SAPIENS (HUMAN), 883.aa	0.00E+00	10

434	cg43297806	973	CCAGGGACAAG ACAGCGGTTCT GCA[G/A]GGAGC GTAGTGCCAGA GGGGTCTGG	G	A	Leu	Leu	SILENT- CODING	sulfotran sferase	Human Gene SWISSPROT- ID:P52849 HEPARIN SULFATE N- DEACETYLASE/N- SULFOTRANSFERASE (EC 2.8.2.-) (N- HSST) (N-HEPARIN SULFATE SULFOTRANSFERASE) (GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE) - HOMO SAPIENS (HUMAN), 883 aa.jpcls:TREMBLNEW-ID:G2792518 HEPARAN GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE-2 - HOMO SAPIENS (HUMAN), 883 aa	0.00E+00	10
435	cg43297806	1004	GTAGTGCCAGA GGGGTCTGGGA GGA[G/A]GCTGA AATCACCTGATA GAAGGTAT	G	A	Ala	Ala	SILENT- CODING	sulfotran sferase	Human Gene SWISSPROT- ID:P52849 HEPARIN SULFATE N- DEACETYLASE/N- SULFOTRANSFERASE (EC 2.8.2.-) (N- HSST) (N-HEPARIN SULFATE SULFOTRANSFERASE) (GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE) - HOMO SAPIENS (HUMAN), 883 aa.jpcls:TREMBLNEW-ID:G2792518 HEPARAN GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE-2 - HOMO SAPIENS (HUMAN), 883 aa	0.00E+00	10

436	cg43297806	1016	GGGTCTGGGAG GAGGCTGAAAT CAC[CT]TGATA GAAGGTATAGTT CAGAGCAA	C	T	Gln	Gln	SILENT- CODING	sulfotran sferase	Human Gene SWISSPROT- ID:P52849 HEPARIN SULFATE N- DEACETYLASE/N- SULFOTRANSFERASE (EC 2.8.2.-) (N- HSST) (N-HEPARIN SULFATE SULFOTRANSFERASE) (GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE) - HOMO SAPIENS (HUMAN), 883 aa.lpcis:TREMBLNEW-ID:G2792518 HEPARAN GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE-2 - HOMO SAPIENS (HUMAN), 883 aa	0.00E+00	10
437	cg43297806	1019	TCTGGGAGGAG GCTGAAATCAC CTG[A/G]TAGAA GGTATAGTTCAG AGCAACTG	A	G	Tyr	Tyr	SILENT- CODING	sulfotran sferase	Human Gene SWISSPROT- ID:P52849 HEPARIN SULFATE N- DEACETYLASE/N- SULFOTRANSFERASE (EC 2.8.2.-) (N- HSST) (N-HEPARIN SULFATE SULFOTRANSFERASE) (GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE) - HOMO SAPIENS (HUMAN), 883 aa.lpcis:TREMBLNEW-ID:G2792518 HEPARAN GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE-2 - HOMO SAPIENS (HUMAN), 883 aa	0.00E+00	10

438	cg43297806	1028	AGGCTGAAATC ACCTGATAGAA GGT[A/G]TAGTT CAGAGCAACTG GGTCTCCAT	A	G	Tyr	Tyr	SILENT- CODING	sulfotran sferase	Human Gene SWISSPROT- ID:P52849 HEPARIN SULFATE N- DEACETYLASE/N- SULFOTRANSFERASE (EC 2.8.2.-) (N- HSST) (N-HEPARIN SULFATE SULFOTRANSFERASE) (GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE) - HOMO SAPIENS (HUMAN), 883 aa.lpcis:TREMBLNEW-ID:G2792518 HEPARAN GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE-2 - HOMO SAPIENS (HUMAN), 883 aa	0.00E+00	10
439	cg43297806	1043	GATAGAAAGGTAT AGTTCAGAGCA ACT[A]GGGTCT CCATGGGCTCG CTGATGCT	T	A	Pro	Pro	SILENT- CODING	sulfotran sferase	Human Gene SWISSPROT- ID:P52849 HEPARIN SULFATE N- DEACETYLASE/N- SULFOTRANSFERASE (EC 2.8.2.-) (N- HSST) (N-HEPARIN SULFATE SULFOTRANSFERASE) (GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE) - HOMO SAPIENS (HUMAN), 883 aa.lpcis:TREMBLNEW-ID:G2792518 HEPARAN GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE-2 - HOMO SAPIENS (HUMAN), 883 aa	0.00E+00	10

440	cg43297806	926	CAGAGGGGTAG TAAGTCAGCCA GCGT/CJGTAG ATGGGTAGAATA GTAGCCAG	T	C	Gln	Gln	SILENT- CODING	sulfotran sferase	Human Gene SWISSPROT- ID:P52849 HEPARIN SULFATE N- DEACETYLASE/N- SULFOTRANSFERASE (EC 2.8.2.-) (N-HSST) (N-HEPARIN SULFATE SULFOTRANSFERASE) (GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE) - HOMO SAPIENS (HUMAN), 883 aa. pcls:TREMBLNEW-ID:G2792518 HEPARAN GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE-2 - HOMO SAPIENS (HUMAN), 883 aa Human Gene Similar to SWISSNEW- ID:P54876 PHOSPHORIBOSYLFORMYLGLYCI NAMIDINE SYNTHASE II (EC 6.3.5.3) (FGAM SYNTHASE II) - MYCOBACTERIUM TUBERCULOSIS, 754 aa.	0.00E+00	10
441	cg39515668	445	CAGCCACATTC CGGTAAGCCTC GCA/A/GJAGGC CAGCTGGGCGC CAAGATACG	A	G	Leu	Leu	SILENT- CODING	synthase	Human Gene Similar to SWISSNEW- ID:P54876 PHOSPHORIBOSYLFORMYLGLYCI NAMIDINE SYNTHASE II (EC 6.3.5.3) (FGAM SYNTHASE II) - MYCOBACTERIUM TUBERCULOSIS, 754 aa.	2.80E-72	
442	cg39515668	538	CGATGCCGAGG TTGTCGTCAATA CG/A/GJATCATG CCGGCATCATT CGGCTGAG	A	G	Ile	Ile	SILENT- CODING	synthase	Human Gene Similar to SWISSNEW- ID:P54876 PHOSPHORIBOSYLFORMYLGLYCI NAMIDINE SYNTHASE II (EC 6.3.5.3) (FGAM SYNTHASE II) - MYCOBACTERIUM TUBERCULOSIS, 754 aa.	2.80E-72	
443	cg39515668	580	TCGGCTGAGCG AGCACAGTATTG CC/A/GJCGCAG AACCGGTCATA CTGGTCGG	A	G	Arg	Arg	SILENT- CODING	synthase	Human Gene Similar to SWISSNEW- ID:P54876 PHOSPHORIBOSYLFORMYLGLYCI NAMIDINE SYNTHASE II (EC 6.3.5.3) (FGAM SYNTHASE II) - MYCOBACTERIUM TUBERCULOSIS, 754 aa.	2.80E-72	

444	cg39515668	655	GGGGGAGCCA ACAAGGGCCAG CAG[G/C]GCCCC AGCAAGACCCT CACCAGAGT	G	C	Ala	Ala	SILENT- CODING	synthase	Human Gene Similar to SWISSNEW- ID:P54876 PHOSPHORIBOSYLFORMYLGLYCI NAMIDINE SYNTHASE II (EC 6.3.5.3) (FGAM SYNTHASE II) - MYCOBACTERIUM TUBERCULOSIS, 754 aa.	2.80E-72	
445	cg21428405	177	TGACCTCGCCA ATGACAGTGGC AGC[G/A]ACACC CCAATGGGCGC AGATCTCCA	G	A	Val	Val	SILENT- CODING	synthase	Human Gene Similar to SWISSNEW- ID:P54876 PHOSPHORIBOSYLFORMYLGLYCI NAMIDINE SYNTHASE II (EC 6.3.5.3) (FGAM SYNTHASE II) - MYCOBACTERIUM TUBERCULOSIS, 754 aa.	2.20E-56	
446	cg21428405	273	CCTGGGACTCG CTCATGAGGAT CTC[T/C]TCAGG GGCAGGTTTCG GGTCGCGCA	T	C	Glu	Glu	SILENT- CODING	synthase	Human Gene Similar to SWISSNEW- ID:P54876 PHOSPHORIBOSYLFORMYLGLYCI NAMIDINE SYNTHASE II (EC 6.3.5.3) (FGAM SYNTHASE II) - MYCOBACTERIUM TUBERCULOSIS, 754 aa.	2.20E-56	
447	cg21428405	327	GAACGCGGTTCG AGCTCGACGTG CAT[G/A]CCACC GTCGCCAGCAC TGCCAGCT	G	A	Gly	Gly	SILENT- CODING	synthase	Human Gene Similar to SWISSNEW- ID:P54876 PHOSPHORIBOSYLFORMYLGLYCI NAMIDINE SYNTHASE II (EC 6.3.5.3) (FGAM SYNTHASE II) - MYCOBACTERIUM TUBERCULOSIS, 754 aa.	2.20E-56	
448	cg38924050	301	TCTCGTTGATGA GGTCGTTACCC TC[A/G]CGGGTA CGTTCACCGAC ACCGCGCA	A	G	Arg	Arg	SILENT- CODING	synthase	Human Gene Similar to SWISSPROT- ID:P50004 ATP SYNTHASE BETA CHAIN (EC 3.6.1.34) - STREPTOMYCES LIVIDANS, 477 aa.	2.60E-53	
449	cg38924050	310	TGAGGTCGTTA CCCTCACGGGT ACG[T/C]TCACC GACACCGCGCA AAACCGAAG	T	C	Glu	Glu	SILENT- CODING	synthase	Human Gene Similar to SWISSPROT- ID:P50004 ATP SYNTHASE BETA CHAIN (EC 3.6.1.34) - STREPTOMYCES LIVIDANS, 477 aa.	2.60E-53	

450	cg38924050	352	AAACCCGAAGTA CCGCCGAAGTT GTG[G/C]GCGAT ACGGTAAATCAT CTCCTGAA	G	C	Ala	Ala	SILENT- CODING	synthase	Human Gene Similar to SWISSPROT- ID:P50004 ATP SYNTHASE BETA CHAIN (EC 3.6.1.34) - STREPTOMYCES LIVIDANS, 477 aa.	2.60E-53	
451	cg43925970	1703	GAGCACATAAG GTGAAGGTGGT GAC[T/A]CCCAG AGAAGCGACCT CTATATAGG	T	A	Gly	Gly	SILENT- CODING	tm7	Human Gene SPTREMBL-ID:O00348 PUTATIVE ENDOTHELIN RECEPTOR TYPE B-LIKE PROTEIN - HOMO SAPIENS (HUMAN), 613 aa.	0.00E+00	9
452	cg41616031	1736	AAGGGATGTCC CCAACTTCCAG TCT[T/C]GAACGC CGCACATAGTA GTCCATCA	T	C	Ser	Ser	SILENT- CODING	tm7	Human Gene SWISSPROT- ID:P49019 PROBABLE G PROTEIN- COUPLED RECEPTOR HM74 - HOMO SAPIENS (HUMAN), 387 aa.	2.90E-214	12
453	cg41616031	1744	TCCCCAAACTTC CAGTCTGAACG CC[G/T]CACATA GTAGTCCATCAC GAACGGC	G	T	Arg	Arg	SILENT- CODING	tm7	Human Gene SWISSPROT- ID:P49019 PROBABLE G PROTEIN- COUPLED RECEPTOR HM74 - HOMO SAPIENS (HUMAN), 387 aa.	2.90E-214	12
454	cg41616031	1796	GGCAGATGATC AGTAGAAAGTCA GCT[T/C]ACTGCC AGGTTGAACAG GAAAATCC	T	C	Val	Val	SILENT- CODING	tm7	Human Gene SWISSPROT- ID:P49019 PROBABLE G PROTEIN- COUPLED RECEPTOR HM74 - HOMO SAPIENS (HUMAN), 387 aa.	2.90E-214	12

455	cg42489842	393	GGCTGGTCAAC ACAGGCTTCTG AC[C/G]CTGCGC CAGATTGTTTG AGCAAAG	C	G	Thr	Thr	SILENT- CODING	tm7	Human Gene Homologous to SWISSPROT-ID:Q02038 NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE) (MITOCHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP) (SOLUBLE ANGIOTENSIN- BINDING PROTEIN) (SABP) - SUS	7.30E-106	
456	cg42489842	402	ACACAGGTCTTC TGACCCCTGCGC CA[G/A]ATTGTTT TGAGCAAAGTT GATCAGT	G	A	Gln	Gln	SILENT- CODING	tm7	Human Gene Homologous to SWISSPROT-ID:Q02038 NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE) (MITOCHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP) (SOLUBLE ANGIOTENSIN- BINDING PROTEIN) (SABP) - SUS	7.30E-106	
457	cg42489842	423	GCCAGATTGTTT TGAGCAAAGTT GAT[C/G]CAGTCT CTTCATACCAAC ACATCGC	T	C	Asp	Asp	SILENT- CODING	tm7	Human Gene Homologous to SWISSPROT-ID:Q02038 NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE) (MITOCHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP) (SOLUBLE ANGIOTENSIN- BINDING PROTEIN) (SABP) - SUS	7.30E-106	

458	cg42489842	432	TTTTGAGCAAAG TTGATCAGTCTC TTT/CJCATACCAA CACATCGCTGG ATGCTG	T	C	Leu	Leu	SILENT- CODING	tm7	Human Gene Homologous to SWISSPROT-ID:Q02038 NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE) (MITOCHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP) (SOLUBLE ANGIOTENSIN- BINDING PROTEIN) (SABP) - SUS	7.30E-106	
459	cg42489842	456	TTCATACCAACA CATCGCTGGAT GC/T/CJGCAAGT GAATATGCCAAA TACTGCT	T	C	Ala	Ala	SILENT- CODING	tm7	Human Gene Homologous to SWISSPROT-ID:Q02038 NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE) (MITOCHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP) (SOLUBLE ANGIOTENSIN- BINDING PROTEIN) (SABP) - SUS	7.30E-106	
460	cg42489842	471	CGCTGGATGCT GCAAGTGAATAT GC/C/TJAAATACT GCTCAGAAATAT TAGGAG	C	T	Ala	Ala	SILENT- CODING	tm7	Human Gene Homologous to SWISSPROT-ID:Q02038 NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE) (MITOCHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP) (SOLUBLE ANGIOTENSIN- BINDING PROTEIN) (SABP) - SUS	7.30E-106	
461	cg42927358	947	TTTTGCTTTTGC CAAACATCATCC TIG/AJACAAATG GTCAGCCCAACA GAGGACA	G	A	Leu	Leu	SILENT- CODING	tm7	SCROFA (PIG), 704 aa. Human Gene Similar to SWISSPROT- ID:Q15391 PROBABLE G PROTEIN- COUPLED RECEPTOR KIAA0001 - HOMO SAPIENS (HUMAN), 338 aa.	1.40E-71	

468	cg43928442	449	CATCCACATGG GCCACGGTGAT GGGIC/AJAGCCC AAAGGCTCCGT ATCTGCAGG	C	A	Leu	Leu	SILENT- CODING	transferase	Human Gene Similar to SPTREMBL-ID:O09034 GLUTATHIONE S-TRANSFERASE SUBUNIT 13 - RATTUS NORVEGICUS (RAT), 226 aa.	2.60E-87	7
469	cg43976701	1859	GACAGCTCATTCA GACTGTGTCAG AA[A/G]TTTGA GAATATCATAAA GATGACC	A	G	Lys	Lys	SILENT- CODING	transport	Human Gene SWISSPROT-ID:Q15436 PROTEIN TRANSPORT PROTEIN SEC23 HOMOLOG ISOFORM A - HOMO SAPIENS (HUMAN), 765 aa.	0.00E+00	
470	cg44005525	975	CTTGACTGTTAA TATTACAATGAT A[G/A]ATTCCTGT CCGAAATGTAAC CTTTG	G	A	Ile	Ile	SILENT- CODING	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P51965 UBIQUITIN-CONJUGATING ENZYME E2-21 KD UBCH6 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 193 aa.	3.30E-101	
471	cg44005525	1041	ATTCCTGGTGTA AAGTGATATCGA G[A/G]AAGAATA CACCACCCCTCAT ACACGG	A	G	Phe	Phe	SILENT- CODING	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P51965 UBIQUITIN-CONJUGATING ENZYME E2-21 KD UBCH6 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 193 aa.	3.30E-101	
472	cg44005525	1047	GTGTAAAAGTGAT TATCGAGAAAGA A[T/G]ACACCAC CCTCATACACG GATCCTG	T	G	Val	Val	SILENT- CODING	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P51965 UBIQUITIN-CONJUGATING ENZYME E2-21 KD UBCH6 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 193 aa.	3.30E-101	
473	cg44005525	1065	GAAGAATACAC CACCCTCATACA C[G/A]GATCCTG GAGGCCCTAGA ATGGTTG	G	A	Ser	Ser	SILENT- CODING	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P51965 UBIQUITIN-CONJUGATING ENZYME E2-21 KD UBCH6 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 193 aa.	3.30E-101	

474	cg44005525	1080	CCTCATACACG GATCCTGGAGG CCCT/CJAGAAT GGTTGATCTCCA TTCATAGA	T	C	Leu	Leu	SILENT- CODING	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P51965 UBIQUITIN- CONJUGATING ENZYME E2-21 KD UBCH6 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 193 aa.	3.30E-101	
475	cg44005525	1098	GAGGCCCTAGA ATGGTTGATCTC CAIT/CJTCATAGA TGTTATCGCCTT TGGGAC	T	C	Glu	Glu	SILENT- CODING	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P51965 UBIQUITIN- CONJUGATING ENZYME E2-21 KD UBCH6 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 193 aa.	3.30E-101	
476	cg44005525	1110	TGGTTGATCTCC ATTCATAGATGT TIA/GJTCGCCITT GGGACCAAGCAC TGCAAT	A	G	Asp	Asp	SILENT- CODING	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P51965 UBIQUITIN- CONJUGATING ENZYME E2-21 KD UBCH6 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 193 aa.	3.30E-101	
477	cg44005525	1134	TATCGCCTTTGG GACCAGCACTG CA[A/G]TTAGGT GGAGGGTCTAA AGTGATGT	A	G	Asn	Asn	SILENT- CODING	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P51965 UBIQUITIN- CONJUGATING ENZYME E2-21 KD UBCH6 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 193 aa.	3.30E-101	
478	cg44005525	828	TGTTGGTCATAT ACTGAGTGGCA AT[A/G]CTTCCC ACCAAAGGGTC GGCAGGAT	A	G	Ser	Ser	SILENT- CODING	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P51965 UBIQUITIN- CONJUGATING ENZYME E2-21 KD UBCH6 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 193 aa.	3.30E-101	

479	cg17663981	225	CCGAGAACCCG GGCACAGCGAG AGC[C/G]TGGTG CCAAAGTGGCCC AAAAGTTCA	C	G	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:Q05329 GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65) (65 KD GLUTAMIC ACID DECARBOXYLASE) - Homo sapiens (Human), 585 aa.	0.00E+00	10 (10p11.2 3)
480	cg17663981	234	CGGGCACAGCG AGAGCCTGGTG CCA[A/G]GTGGC CCAAAGTTTAC GGCGGGCA	A	G	Gln	Gln	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:Q05329 GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65) (65 KD GLUTAMIC ACID DECARBOXYLASE) - Homo sapiens (Human), 585 aa.	0.00E+00	10 (10p11.2 3)
481	cg42907760	1501	AACCTGAAGGC CAAAGTGTGAC TC[G/A]GACTCG GAGAGCACAGT CAGCCCCC	G	A	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q15464 SHB MRNA - HOMO SAPIENS (HUMAN), 596 aa.	0.00E+00	9 (9p12)
482	cg43301812	3795	CTCCATGGCTG GGATGCTCTGC TGC[G/A]CTTGG TTTTGCCCGAGT GGCAGCCT	G	A	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:Q93075 HYPOTHETICAL PROTEIN KIAA0218 - Homo sapiens (Human), 761 aa.	0.00E+00	3
483	cg43917756	1098	AGACACTGACC ACTGGGGGAGG TGC[A/G]GAGAC TGTGCTGGATG TGGTGGAAA	A	G	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:Q14157 HYPOTHETICAL PROTEIN KIAA0144 - Homo sapiens (Human), 983 aa.	0.00E+00	1
484	cg43918356	2645	CATCTTCATCTA GAAACGCCCTC AC[G/T]GAAATG GAATTGCTGCC AGACGTGG	G	T	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O75176 KIAA0692 PROTEIN - HOMO SAPIENS (HUMAN), 783 aa (fragment).	0.00E+00	12

485	cg43924089	1031	CTGTGGTCTCT CCACAGACAGG GTCTTCACATC AAACTGGGGT GTCTCCAC	C	T	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA31589 KIAA0614 PROTEIN + HOMO SAPIENS (HUMAN), 1630 aa (fragment).	0.00E+00	12
486	cg43926428	2157	CAAACTTCATGA GATTGAAGATCT GTC/GIAGCTGCT GCTCCTTGAACA TGCTCTG	C	G	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW- ACC:O14924 REGULATOR OF G- PROTEIN SIGNALING 12 (RGS12) - Homo sapiens (Human), 1447 aa.	0.00E+00	4
487	cg43950657	2478	CCTCTACCCATC GGTCAGTGTC CC[A/G]CCACCG GGGGCTGCTG GGACTCTT	A	G	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW- ACC:Q13009 T-LYMPHOMA INVASION AND METASTASIS INDUCING PROTEIN 1 (TIAM1 PROTEIN) - Homo sapiens (Human), 1591 aa.	0.00E+00	21 (21q22.1)
488	cg43955358	3560	CCCGACAATTGT ATCTGGCATAAA TTC/TCCCTTCACC CAGTAGATTAG GAATGA	C	T	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW- ACC:P35573 GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA- GLUCANOTRANSFERASE (EC 2.4.1.25) (OLIGO-1,4-1,4- GLUCANTRANSFERASE) AMYLO- 1,6-GLUCOSIDASE (EC 3.2.1.33) (DEXTRIN 6-ALPHA-D- GLUCOSIDASE)] - Homo sapiens (Human), 1515 aa.	0.00E+00	1 (1p21)
489	cg43970200	1374	CATTAGAGATCT GGGCTGCAAGG TC[C/T]CCAACAT AATCAATAAACA GATTTT	C	T	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q92845 SMAP - HOMO SAPIENS (HUMAN), 792 aa.	0.00E+00	1
490	cg43970200	1629	TTAACTGTGGTA TACAGTCAGTGT AT[C/G]GCAACA TTGATTTAAAGC GGTCAT	T	C	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q92845 SMAP - HOMO SAPIENS (HUMAN), 792 aa.	0.00E+00	1

491	cg43999667	3688	GTACAGCCTGG TAATGGAGAATC AA[A/G]TTTGTCT GTATCGTAAAG GCAGCAA	A	G	Asn	Asn	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O60281 KIAA0530 PROTEIN - HOMO SAPIENS (HUMAN), 1563 aa (fragment).	0.00E+00	6
492	cg44009187	6789	TCAACTTGCTCC AGTAGGCCGCC GG[C/T]TCTGCA GGCAGCTCGGG CTGGAAGA	C	T	Glu	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:P42858 HUNTINGTIN (HUNTINGTON'S DISEASE PROTEIN) (HD PROTEIN) - Homo sapiens (Human), 3144 aa.	0.00E+00	
493	cg44020180	3172	ATGGGTAGACT CGAGTTTGGTAA AT[G/A]TCCAAA CCATAGGCCAC AACCAAAC	G	A	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q14700 MRNA (KIAA0090) FOR ORF (RELATED TO YEAST GENE IN CHROMOSOME III) - HOMO SAPIENS (HUMAN), 905 aa (fragment).	0.00E+00	1
494	cg44020180	3177	TAGACTCGAGTT TGGTAAATGTCC A[A/G]ACCATAG GCCACAACCAA ACAAAGTG	A	G	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q14700 MRNA (KIAA0090) FOR ORF (RELATED TO YEAST GENE IN CHROMOSOME III) - HOMO SAPIENS (HUMAN), 905 aa (fragment).	0.00E+00	1
495	cg44020180	3199	CCAAACCATAG GCCACAACCAA ACA[A/T]GTGGA CTCCAGACCCG AGGGAGCTG	A	T	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q14700 MRNA (KIAA0090) FOR ORF (RELATED TO YEAST GENE IN CHROMOSOME III) - HOMO SAPIENS (HUMAN), 905 aa (fragment).	0.00E+00	1
496	cg44020180	3211	CCACAACCAA CAAGTGGACTC CAG[A/G]CCCCGA GGGAGCTGTGT AGATACCTC	A	G	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q14700 MRNA (KIAA0090) FOR ORF (RELATED TO YEAST GENE IN CHROMOSOME III) - HOMO SAPIENS (HUMAN), 905 aa (fragment).	0.00E+00	1

497	cg44020180	3220	AACAAAGTGGAC TCCAGACCCGA GGG[A/C]GCTGT GTAGATACCTC GCATTCGAG	A	C	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q14700 MRNA (KIAA0090) FOR ORF (RELATED TO YEAST GENE IN CHROMOSOME III) - HOMO SAPIENS (HUMAN), 905 aa (fragment).	0.00E+00	1
498	cg44020180	3226	TGGAATCCAGA CCCGAGGGAGC TGT[G/A]TAGATA CCTCGCATTCG AGAAACTG	G	A	Tyr	Tyr	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q14700 MRNA (KIAA0090) FOR ORF (RELATED TO YEAST GENE IN CHROMOSOME III) - HOMO SAPIENS (HUMAN), 905 aa (fragment).	0.00E+00	1
499	cg44020180	3232	CCAGACCCGAG GGAGCTGTGTA GAT[A/G]CCTCG CATTGAGAAAC TGCTCTGGT	A	G	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q14700 MRNA (KIAA0090) FOR ORF (RELATED TO YEAST GENE IN CHROMOSOME III) - HOMO SAPIENS (HUMAN), 905 aa (fragment).	0.00E+00	1
500	cg44020180	3247	CTGTGTAGATAC CTCGCATTCGA GA[A/G]ACTGTC TGGTTATAGTTG ATGAATC	A	G	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q14700 MRNA (KIAA0090) FOR ORF (RELATED TO YEAST GENE IN CHROMOSOME III) - HOMO SAPIENS (HUMAN), 905 aa (fragment).	0.00E+00	1
501	cg44020180	3289	TGATGAATCGCT CTGCGTGTATCT G[T/G]ACATCTG GAGAATACGGG ATTAAGT	T	G	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q14700 MRNA (KIAA0090) FOR ORF (RELATED TO YEAST GENE IN CHROMOSOME III) - HOMO SAPIENS (HUMAN), 905 aa (fragment).	0.00E+00	1
502	cg44020180	3298	GCTCTGCGTGT ATCTGTACATCT GG[A/G]GAATAC GGGATTAAAGTTC TCCTCTC	A	G	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q14700 MRNA (KIAA0090) FOR ORF (RELATED TO YEAST GENE IN CHROMOSOME III) - HOMO SAPIENS (HUMAN), 905 aa (fragment).	0.00E+00	1

503	cg44020180	3312	TGTACATCTGGA GAATACGGGAT TA[AG]GTTCTC CTCTCTGCTTTG TTCTGTT	A	G	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q14700 MRNA (KIAA0090) FOR ORF (RELATED TO YEAST GENE IN CHROMOSOME III) - HOMO SAPIENS (HUMAN), 905 aa (fragment).	0.00E+00	1
504	cg44020180	3319	CTGGAGAATAC GGGATTAAGTTC TC[C/TT]CTCTGC TTTGTTCTGTTG GGATCT	C	T	Glu	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q14700 MRNA (KIAA0090) FOR ORF (RELATED TO YEAST GENE IN CHROMOSOME III) - HOMO SAPIENS (HUMAN), 905 aa (fragment).	0.00E+00	1
505	cg44928323	2080	AGCAGGCAGAT AGAAGTTCCTGT CA[C/TT]TTTCTCC TTTTTACGGGG TAGGAT	C	T	His	His	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:P97526 NEUROFIBROMIN - RATTUS NORVEGICUS (RAT), 2820 aa.	0.00E+00	17 (17q11.2)
506	cg44932392	1281	TGCTTGGTTTT TGATAAAATTGT T[G/A]AACTTATT GTTGAGATCAG CGCTGA	G	A	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD23581 CULLIN 2 - HOMO SAPIENS (HUMAN), 745 aa.	0.00E+00	
507	cg43991434	1266	TC TTGAGCAGA CCCATGTGCAC GAG[G/C]AGCCT GGTGAGGAAAGG TGTTGGAGT	G	C	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW- ACC:P46060 RAN-GTPASE ACTIVATING PROTEIN 1 - Homo sapiens (Human), 587 aa.	1.70E-304	22
508	cg43985955	1994	GCATGATAGGA TATGGAATTCCT CC[AT]CAAATG GGAAGTGTTCC TGTAATGA	A	T	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q13492 CALM (TYPE I CALM PROTEIN) - HOMO SAPIENS (HUMAN), 652 aa.	2.70E-299	
509	cg43985955	2009	GAATTCCTCCAC AAATGGGAAGT GTT[AT]CCTGTAA TGACGCAACCA ACCTTAA	T	A	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q13492 CALM (TYPE I CALM PROTEIN) - HOMO SAPIENS (HUMAN), 652 aa.	2.70E-299	

510	cg43985955	2021	AAATGGGAAGT GTTCTCTGTAATG AC[G/A]CAACCA ACCTTAATATAC AGCCAGC	G	A	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q13492 CALM (TYPE I CALM PROTEIN) - HOMO SAPIENS (HUMAN), 652 aa.	2.70E-299	
511	cg43985955	2060	TATACAGCCAG CCTGTGTCATGAG ACC[T/G]CCAAA CCCCITTTGGCC CTGTATCAG	T	G	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q13492 CALM (TYPE I CALM PROTEIN) - HOMO SAPIENS (HUMAN), 652 aa.	2.70E-299	
512	cg44031765	2070	ACCTCGCCGTA GTAGATGTAGC GCA[G/A]CATGG ACTCGAAGGCC TGCCTGCTG	G	A	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q14776 LZTR-1 - HOMO SAPIENS (HUMAN), 552 aa.	4.60E-279	22
513	cg43252100	466	TGCAGCCCCAGA GGTCTCTTTTAC TC[C/A]ATGGTA CCAAATGCAACT ATTACCC	C	A	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA83037 KIAA1085 PROTEIN HOMO SAPIENS (HUMAN), 584 aa (fragment).	4.90E-278	
514	cg43934178	2445	CGATGCCATGC TTCTCCATGAGC GT[G/A]ATGAGC TCGGCCTCCGT CAGGTAGT	G	A	Ile	Ile	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD29670 DNA TOPOISOMERASE III BETA - HOMO SAPIENS (HUMAN), 862 aa.	1.80E-274	
515	cg43031103	1696	ACATGGCCCTC CCCTTGTTGA GGA[G/A]ACAGC AGGGCTGGTG TGAGGTGCA	G	A	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O60240 PERILIPIN - HOMO SAPIENS (HUMAN), 522 aa.	6.30E-266	
516	cg43258841	340	TAAATCTTGTGT GGCCATCATCC AGT[G]GTGTGG AACATTTACCG TCATCTT	T	G	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW- ACC:Q14449 GROWTH FACTOR RECEPTOR-BOUND PROTEIN 14 (GRB14 ADAPTER PROTEIN) - Homo sapiens (Human), 540 aa.	2.70E-258	

517	cg43258841	358	CATCCAGTGTGT GGAACATTTTCAC C[G/A]TCATCTTC TACTGGTATAAT TTGAA	G	A	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW- ACC:Q14449 GROWTH FACTOR RECEPTOR-BOUND PROTEIN 14 (GRB14 ADAPTER PROTEIN) - Homo sapiens (Human), 540 aa.	2.70E-258	
518	cg43258841	370	GGAACATTTTCAC CGTCATCTTCTA CTT[G/G]GGTATAA TTTGAAGTGCT TTATTT	T	G	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW- ACC:Q14449 GROWTH FACTOR RECEPTOR-BOUND PROTEIN 14 (GRB14 ADAPTER PROTEIN) - Homo sapiens (Human), 540 aa.	2.70E-258	
519	cg43258841	388	CTTCTACTGGTA TAATTTGAAAGT G[C/T]TTTATTTT TTGTCCATGACT CATTG	C	T	Lys	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW- ACC:Q14449 GROWTH FACTOR RECEPTOR-BOUND PROTEIN 14 (GRB14 ADAPTER PROTEIN) - Homo sapiens (Human), 540 aa.	2.70E-258	
520	cg43258841	394	CTGGTATAATTT GAAAGTGCTTTA TTT[C/T]TTTGTCC ATGACTCATTGA CAGTA	T	C	Lys	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW- ACC:Q14449 GROWTH FACTOR RECEPTOR-BOUND PROTEIN 14 (GRB14 ADAPTER PROTEIN) - Homo sapiens (Human), 540 aa.	2.70E-258	
521	cg43258841	403	TTTGAAAGTGCT TTATTTTGTGTC C[A/G]TGACTCA TTGACAGTACGA AAGTTT	A	G	His	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW- ACC:Q14449 GROWTH FACTOR RECEPTOR-BOUND PROTEIN 14 (GRB14 ADAPTER PROTEIN) - Homo sapiens (Human), 540 aa.	2.70E-258	
522	cg43258841	421	TTTGTCATGAC TCATTGACAGTA C[G/A]AAAAGTTT GGGGTTACTCT GACTAT	G	A	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW- ACC:Q14449 GROWTH FACTOR RECEPTOR-BOUND PROTEIN 14 (GRB14 ADAPTER PROTEIN) - Homo sapiens (Human), 540 aa.	2.70E-258	
523	cg43258841	484	AAACTCCATCCA CAAGTCCTTGCT G[A/G]ATAATCA ATCGCTGAGCC TCATCTC	A	G	Ile	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW- ACC:Q14449 GROWTH FACTOR RECEPTOR-BOUND PROTEIN 14 (GRB14 ADAPTER PROTEIN) - Homo sapiens (Human), 540 aa.	2.70E-258	
524	cg43258841	493	CCACAAGTCCTT GCTGAATAATCA AT[C/G]CGCTGAG CCTCATCTCTAG AAATTT	T	C	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW- ACC:Q14449 GROWTH FACTOR RECEPTOR-BOUND PROTEIN 14 (GRB14 ADAPTER PROTEIN) - Homo sapiens (Human), 540 aa.	2.70E-258	

525	cg43971614	2529	TCACITTCCTGT GGATTTCCTTCT GTT/CJCCGTAGA CTGCATCTGCT GGCTTTC	T	C	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q13283 GAP SH3 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 466 aa.	5.30E-253	5
526	cg43971614	2574	GCTTCCATTG AATCCAATCCCC CJA/GJTGACAT AAGAAGAGTTCT TTCCAT	A	G	His	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q13283 GAP SH3 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 466 aa.	5.30E-253	5
527	cg43320405	916	TGTTCTTCAGGC CCTTCACCATG GAJA/GJGGCAGG AGGGCCTTCAC CTTGCGGG	A	G	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB46424 DKFZP434G153 PROTEIN - HOMO SAPIENS (HUMAN), 466 aa.	8.20E-245	
528	cg43922856	1667	TTACTGGACCAT CTATACGAAAT GTT/CJCTCTGAAG TTTCCACCCCTTT TCCTTG	T	C	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:P42167 THYMOPOIETINS BETA AND GAMMA (TP BETA AND TP GAMMA) - Homo sapiens (Human), 453 aa.	2.00E-237 (12q22)	12
529	cg43922856	1718	GAGTCTCTCTTG ACCCTCTTGTAG ATT/CJTCCTTAGT TAATGCTGCA GAGGTC	T	C	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:P42167 THYMOPOIETINS BETA AND GAMMA (TP BETA AND TP GAMMA) - Homo sapiens (Human), 453 aa.	2.00E-237 (12q22)	12
530	cg43991007	102	CAAGAGAACAG CAAGTGCACCA AACIT/CJTAGCT GAAACAGAAAA GAGACAGC	T	C	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O75336 LIPIN-BETA1 - HOMO SAPIENS (HUMAN), 1005 aa.	1.80E-236	
531	cg43940463	1709	GGCTCACCAGC TCCAGCTGCGT GTGTT/CJTCATC CACCACCAGCG TGTACTTGA	T	C	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q99771 JIP-1 - HOMO SAPIENS (HUMAN), 467 aa.	3.10E-232	

532	cg42676981	1712	GGAAGTAGAGG TCAGGTGGGC TGT[G/A]GGCT CTTCAGGTTCAA ACACCGGA	G	A	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:P08910 PROTEIN PHPS1-2 - Homo sapiens (Human), 425 aa.	5.90E-231	15
533	cg43918561	843	GGAAGGAGGTC TACACCACGCT GAA[G/A]GGCCT CTACGCCACGC ACGCCCTGCG	G	A	Lys	Lys	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:P04177 TYROSINE 3- MONOOXYGENASE (EC 1.14.16.2) (TYROSINE 3-HYDROXYLASE) (TH) Rattus norvegicus (Rat), 498 aa.	2.10E-224 (11p15.5)	11
534	cg43999712	566	ACGTACCAATG AAATGCTCTACG G[G/C]CGAATAG GCTACATCTATG CTCTGC	G	C	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O43813 SEVENTRANSMEMBRANE-DOMAIN PROTEIN - HOMO SAPIENS (HUMAN), 399 aa.	3.30E-221	2
535	cg43999712	569	TACCAATGAAA TGCTCTACGGG CG[A/C]ATAGGC TACATCTATGCT CTGCTTT	A	C	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O43813 SEVENTRANSMEMBRANE-DOMAIN PROTEIN - HOMO SAPIENS (HUMAN), 399 aa.	3.30E-221	2
536	cg43999712	659	GCCATATTCAGC AGATTGTGAAA C[A/C]ATTTTAAAC CTCTGGAGAAA ACCTAT	A	C	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O43813 SEVENTRANSMEMBRANE-DOMAIN PROTEIN - HOMO SAPIENS (HUMAN), 399 aa.	3.30E-221	2
537	cg43922139	1860	ACTTGACTTTCC AGACACGGTGA GG[A/G]AGGAGG AGGCTGTCGGG ACCAAACG	A	G	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O88473 RJS - MUS MUSCULUS (MOUSE), 4836 aa.	2.80E-218	
538	cg43955639	512	CAGGCATGGTG ATGAGGGGTGC TGG[G/T]GCCAG GGAGGTGGCAG GAGCTGGCA	G	T	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O15417 CAGL79 - HOMO SAPIENS (HUMAN), 413 aa (fragment).	2.80E-215	

539	cg41022625	1066	GCCTGGCCATT GTCATCTTCTTC TC/T/CJGTGCTG GGCGTGGTCTT TGGCAAAG	T	C	Ser	Silent- Coding	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34036 CGI-40 PROTEIN - HOMO SAPIENS (HUMAN), 845 aa.	2.00E-207	11
540	cg41022625	1102	TGGTCTTTGGCA AAGGGAACACG GC/G/CJTCTGG ATCGTCTTCTCC ATCATT	G	C	Ala	Silent- Coding	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34036 CGI-40 PROTEIN - HOMO SAPIENS (HUMAN), 845 aa.	2.00E-207	11
541	cg41022625	1111	GCAAAGGGAAC ACGGCGTTCTG GATC/TJGTCTTC TCCATCATTCAC ATCATCG	C	T	Ile	Silent- Coding	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34036 CGI-40 PROTEIN - HOMO SAPIENS (HUMAN), 845 aa.	2.00E-207	11
542	cg44002669	1439	CCTTGGCGTTG CACTCGCGGCA GCC/C/TJCTGTC CAGTTCCTCCTT CTCCTTCT	C	T	Arg	Silent- Coding	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q16543 CDC37 HOMOLOG - HOMO SAPIENS (HUMAN), 378 aa.	8.80E-205	
543	cg43302693	702	CCCCACCTGA GTGACAATGAT GTA/T/CJTTGAC CCCACCGGGGG TCGGCTCCA	T	C	Lys	Silent- Coding	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:P53602 DIPHOSPHOMEVALONATE DECARBOXYLASE (EC 4.1.1.33) (MEVALONATE PYROPHOSPHATE DECARBOXYLASE) - Homo sapiens (Human), 400 aa.	2.70E-204	16
544	cg43921081	486	ACTTGAAAGAA AGTATGCAGCG CT/A/GJTACCCAG CCTCTCTTTGAC AAGAGAA	A	G	Leu	Silent- Coding	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:Q99733 NUCLEOSOME ASSEMBLY PROTEIN 1-LIKE 4 (NUCLEOSOME ASSEMBLY PROTEIN 2) (NAP2) - Homo sapiens (Human), 375 aa.	3.10E-202	11
545	cg42181143	1134	CACACCCAGCG TTCTGCCACTCC GAT/CJCCAAAG AAACTATGATCT TTGCTTT	T	C	Gly	Silent- Coding	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O15268 SKAP55 PROTEIN - HOMO SAPIENS (HUMAN), 359 aa.	2.80E-189	17

546	cg43918701	1667	TTTTCCAGATGC GACAGACATCAT TTTC/GGGCATA TTCTAGAAACCA AGGGCA	T	C	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O60736 KE03 PROTEIN - HOMO SAPIENS (HUMAN), 367 aa (fragment).	1.10E-170	
547	cg43926685	815	AGAATTCCCTTAC TGATCACCGC AACTTAAGACC ATCCACAACGAT TACCGCA	C	T	Asn	SILENT- CODING	UNCLAS SIFIED	Human Gene SWISSNEW- ACC:P23280 CARBONIC ANHYDRASE VI PRECURSOR (EC 4.2.1.1) (CARBONATE DEHYDRATASE VI) - Homo sapiens (Human), 308 aa.	2.50E-168 (1p36.33)	1
548	cg44927654	263	GTGCCAGCTTC TCCATGGTGGC ATCCT/GTCAG GATGCTGGGGT AGGGAGGTT	C	T	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA74865 KIAA0842 PROTEIN - HOMO SAPIENS (HUMAN), 1020 aa (fragment).	7.3E-165	
549	cg43993462	2019	CCAACTCATTGA CAGTGAGGGGT GC[G/A]TCTCCA CTTCTGTTGGTG TAATTGA	G	A	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q63965 TRICARBOXYLATE CARRIER - RATTUS NORVEGICUS (RAT), 357 aa (fragment).	5.1E-161	5
550	cg44010310	1180	CTATATTCTCTG ATTGTGCAAGT A/C/TAGGACAT TATATTCGACAT CTTTGG	C	T	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA32101 BCAP - HOMO SAPIENS (HUMAN), 331 aa.	1.3E-155	13
551	cg43950590	1319	GGTGCAACCATG TACAGCTGCC AATC/TGTGAGA GAAGAATCCTC CGACGGCTT	C	T	Gln	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O75323 GBAS - HOMO SAPIENS (HUMAN), 286 aa.	1.9E-154	7
552	cg43950590	1334	GCTGCCCAATC TGAGAGAAAGAA TCC/T/CCCGAC GGCTTCGTTAC CATCCTGTC	T	C	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O75323 GBAS - HOMO SAPIENS (HUMAN), 286 aa.	1.90E-154	7

553	cg43950590	1361	CGACGGCTTCG TTACCATCCTGT CT[G/A]AGCGG ATTGCACGAGC CCAGTAAT	G	A	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O75323 GBAS - HOMO SAPIENS (HUMAN), 286 aa.	1.90E-154	7
554	cg43950590	1370	CGTTACCATCCT GTCCTGAAGCGG ATT[G]GCACGA GCCCAGTAATT GCCCCATT	T	G	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O75323 GBAS - HOMO SAPIENS (HUMAN), 286 aa.	1.90E-154	7
555	cg43950590	1376	CATCCTGTCTGA AGCGGATTGCA CG[A/G]GCCCCAG TAATTGCCCCAT TCAATCA	A	G	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O75323 GBAS - HOMO SAPIENS (HUMAN), 286 aa.	1.90E-154	
556	cg43950590	1397	CACGAGCCCCAG TAATTGCCCCAT TC[A/G]ATCATG GTTCCCTGGTCG GAGTTGGT	A	G	Ile	Ile	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O75323 GBAS - HOMO SAPIENS (HUMAN), 286 aa.	1.90E-154	7
557	cg43950590	1436	GTCGGAGTTGG TAAGACCTGAGT TC[A/G]TATATAT TAGGTCCGGAT CTTGGCA	A	G	Tyr	Tyr	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O75323 GBAS - HOMO SAPIENS (HUMAN), 286 aa.	1.90E-154	7
558	cg43950590	1445	GGTAAGACCTG AGTTCATATATA TT[A/G]GGTCCG GATCTTGGCAC AGGCTCAT	A	G	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O75323 GBAS - HOMO SAPIENS (HUMAN), 286 aa.	1.90E-154	7
559	cg43951092	1484	GAGTAGAATTCA AGAAGAGTTCAA T[A/G]TATCGAT GTTGCATGTTAT TTTTAT	A	G	Tyr	Tyr	SILENT- CODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD45179 RIBONUCLEOPROTEIN - HOMO SAPIENS (HUMAN), 346 aa.	4.50E-152	14

567	cg43986914	319	TCAGGAAAAGG AAGCATGACAAT TTCTCCTCCACATA ACCAAAGAAAGA GAAGGGA	C	T	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q99598 TRANSLIN-ASSOCIATED PROTEIN X (TRANSLIN-ASSOCIATED FACTOR X) - Homo sapiens (Human), 290 aa.	2.10E-148	
568	cg43119818	1245	AAGAAATTATCA ATGTGGGGCAT TCCTCCTCCATG TAAATTTTGAGG ACAACG	T	C	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P00915 CARBONIC ANHYDRASE I (EC 4.2.1.1) (CARBONATE DEHYDRATASE I) - Homo sapiens (Human), 260 aa.	6.90E-141	8 (8q22)
569	cg44027444	681	CAGTGCCAGAG TCCAGGAACCTG AACAGTCAAG AGCCCGGCTGC TGTGAACAT	A	G	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:BAA76379 TUDOR REPEAT ASSOCIATOR WITH PCTAIRE 2 - HOMO SAPIENS (HUMAN), 468 aa (fragment).	2.50E-129	9
570	cg29351416	429	CCACACAGGAC ACTGTGGTGCC CCTTCCTGATGC TCTGTCCAAATA CGGAGCAG	T	C	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q03626 ALPHA-1- INHIBITOR III PRECURSOR, ISOFORM 2 (RAT PLASMA PROTEINASE INHIBITOR ALPHA-1- INHIBITOR III GROUP 3 VARIANT 36A) (ALPHA-1 PROTEINASE INHIBITOR 3, EXONS 1-4) - RATTUS NORVEGICUS (RAT), 1487 aa.	3.20E-127	
571	cg29351416	435	AGGACACTGTG GTGGCCCTTGA TGCCTCCTGTC CAAATACGGAG CAGCTACTT	T	C	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q03626 ALPHA-1- INHIBITOR III PRECURSOR, ISOFORM 2 (RAT PLASMA PROTEINASE INHIBITOR ALPHA-1- INHIBITOR III GROUP 3 VARIANT 36A) (ALPHA-1 PROTEINASE INHIBITOR 3, EXONS 1-4) - RATTUS NORVEGICUS (RAT), 1487 aa.	3.20E-127	

576	cg44930828	555	TCAACACAAGG CAGCCACAGGC CAA[AG]ATCATT GTATTGGGTTTG TTACCTC	A	G	Lys	Lys	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q29459 PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE IB BETA SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 30 KD SUBUNIT) (PAF-AH 30 KD SUBUNIT) (PAF-AH BETA SUBUNIT) - Homo sapiens (Human), and Bos taurus (Bovine), 229 aa.	3.10E-122	
577	cg44930828	564	GGCAGCCACAG GCCAAATCATT GT[AG]TTGGGT TTGTTACCTCGA GGTGAGA	A	G	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q29459 PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE IB BETA SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 30 KD SUBUNIT) (PAF-AH 30 KD SUBUNIT) (PAF-AH BETA SUBUNIT) - Homo sapiens (Human), and Bos taurus (Bovine), 229 aa.	3.10E-122	
578	cg44930828	591	TGGGTTTGTAC CTCGAGGTGAG AA[AG]CCCAAT CCTTGAGGCA AAAGAACG	A	G	Lys	Lys	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q29459 PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE IB BETA SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 30 KD SUBUNIT) (PAF-AH 30 KD SUBUNIT) (PAF-AH BETA SUBUNIT) - Homo sapiens (Human), and Bos taurus (Bovine), 229 aa.	3.10E-122	
579	cg44930828	597	TGTTACCTCGAG GTGAGAAACCC AA[T/C]CCCTTTGA GGCAAAAGAAC GCCAAGG	T	C	Asn	Asn	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q29459 PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE IB BETA SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 30 KD SUBUNIT) (PAF-AH 30 KD SUBUNIT) (PAF-AH BETA SUBUNIT) - Homo sapiens (Human), and Bos taurus (Bovine), 229 aa.	3.10E-122	

580	cg44930828	603	CTCGAGGTGAG AAACCCCAATCCT TT[G/A]AGGCAA AAGAACGCCAA GGTGAACC	G	A	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q29459 PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE IB BETA SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 30 KD SUBUNIT) (PAF-AH 30 KD SUBUNIT) (PAF-AH BETA SUBUNIT) - Homo sapiens (Human), and Bos taurus (Bovine). 229 aa.	3.10E-122	
581	cg44930828	615	AACCCCAATCCTT TGAGGCCAAAAG AA[C/T]GCCAAG GTGAACCAACT CCTCAAGG	C	T	Asn	Asn	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q29459 PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE IB BETA SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 30 KD SUBUNIT) (PAF-AH 30 KD SUBUNIT) (PAF-AH BETA SUBUNIT) - Homo sapiens (Human), and Bos taurus (Bovine). 229 aa.	3.10E-122	
582	cg44930828	630	GGCAAAAGAAC GCCAAGGTGAA CCA[A/G]CTCCT CAAGTTTCGCT GCCGAAGC	A	G	Gln	Gln	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q29459 PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE IB BETA SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 30 KD SUBUNIT) (PAF-AH 30 KD SUBUNIT) (PAF-AH BETA SUBUNIT) - Homo sapiens (Human), and Bos taurus (Bovine). 229 aa.	3.10E-122	
583	cg44930828	645	AGGTGAACCAA CTCCTCAAGTT TC[G/C]CTGCCG AAGCTTGCCAA CGTGCAGC	G	C	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q29459 PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE IB BETA SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 30 KD SUBUNIT) (PAF-AH 30 KD SUBUNIT) (PAF-AH BETA SUBUNIT) - Homo sapiens (Human), and Bos taurus (Bovine). 229 aa.	3.10E-122	

584	cg44930828	663	AGGTTTCGCTG CCGAAGCTTGC CAA[C/T]GTGCA GCTCCTGGATA CCGACGGGG	C	T	Asn	Asn	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q29459 PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE IB BETA SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 30 KD SUBUNIT) (PAF-AH 30 KD SUBUNIT) (PAF-AH BETA SUBUNIT) - Homo sapiens (Human), and Bos taurus (Bovine), 229 aa.	3.10E-122	
585	cg44930828	690	TGCAGCTCCTG GATACCGACGG GGG[T/C]TTTGT GCACTCGGACG GTGCCATCT	T	C	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q29459 PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE IB BETA SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 30 KD SUBUNIT) (PAF-AH 30 KD SUBUNIT) (PAF-AH BETA SUBUNIT) - Homo sapiens (Human), and Bos taurus (Bovine), 229 aa.	3.10E-122	
586	cg44930828	693	AGCTCCTGGAT ACCGACGGGG TTT[T/C]GTGCAC TCGGACGGTGC CATCTCCT	T	C	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q29459 PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE IB BETA SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 30 KD SUBUNIT) (PAF-AH 30 KD SUBUNIT) (PAF-AH BETA SUBUNIT) - Homo sapiens (Human), and Bos taurus (Bovine), 229 aa.	3.10E-122	
587	cg43975478	691	AAAACCTGAG AAAAGATACAAT GT[C/T]CTGGGA GCTGAGACTGT GCTCAATC	C	T	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q63555 SP120 - RATTUS NORVEGICUS (RAT), 798 aa.	4.10E-119	
588	cg42530218	601	GCATGCCCAGT AATAAAGATGAA GAT[C/G]GGGCTA GTGGTTTGTAGTT TTCAACA	T	C	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P70582 NUCLEOPORIN P54 - RATTUS NORVEGICUS (RAT), 510 aa.	2.00E-118	

589	cg4312211	248	AGTGGTGGATC CCCAGGAGGAG GAG[C/A]GAAGG CGGGCAGGTGG CGGGGCAGA	C	A	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O43770 BCL7C PROTEIN - HOMO SAPIENS (HUMAN), 217 aa.	5.00E-115	
590	cg43986282	656	CTTTGGCCCAT ACTTCTTTCCGT A[G/A]CAGGATT TGCAGTAGATCT CTTCAT	G	A	Cys	Cys	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P97314 DOUBLE LIM PROTEIN-1 - MUS MUSCULUS (MOUSE), 193 aa.	2.90E-110	12
591	cg43986282	683	AGGATTGCAGT AGATCTCTTCAT C[G/A]TGAATTG CCACTGTTGTG CTATCTA	G	A	His	His	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P97314 DOUBLE LIM PROTEIN-1 - MUS MUSCULUS (MOUSE), 193 aa.	2.90E-110	12
592	cg43986282	704	CATCGTGAATTG CCACTGTTGTG CT[A/G]TCTAAAT TTTTCCTGCAAA CCATGC	A	G	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P97314 DOUBLE LIM PROTEIN-1 - MUS MUSCULUS (MOUSE), 193 aa.	2.90E-110	12
593	cg43986282	731	CTAAATTTTCC TGCAAACCATG CA[G/C]AGAAAG CAGCAGCGGTG GAAGCTCC	G	C	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P97314 DOUBLE LIM PROTEIN-1 - MUS MUSCULUS (MOUSE), 193 aa.	2.90E-110	12
594	cg43986282	757	AGAAAGCAGCA GCGGTGGAAGC TCC[T/G]GCCAT CACACTGCACC TCTTCTGCG	T	G	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P97314 DOUBLE LIM PROTEIN-1 - MUS MUSCULUS (MOUSE), 193 aa.	2.90E-110	12
595	cg43986282	779	TCCTGCCATCAC ACTGCACCTCTT CT[A/G]CGTGGT ACACGGTCCTC CCACAGG	T	A	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P97314 DOUBLE LIM PROTEIN-1 - MUS MUSCULUS (MOUSE), 193 aa.	2.90E-110	12

596	cg43986282	794	GCACCTCTTCTG CGTGGTACACG GT[C/T]CTCCCA CAGGCCCCACA CTTGTTTC	C	T	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P97314 DOUBLE LIM PROTEIN-1 - MUS MUSCULUS (MOUSE), 193 aa.	2.90E-110	12
597	cg43986282	800	CTTCTGCGTGG TACACGGTCCT CCG[A/G]CAGGC CCACACTTGTT TCCACCTC	A	G	Cys	Cys	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P97314 DOUBLE LIM PROTEIN-1 - MUS MUSCULUS (MOUSE), 193 aa.	2.90E-110	12
598	cg43986282	809	GGTACACGGTC CTCCACACAGC CCG[A/G]CACTT GTTCCACCTCC CCAGACAG	A	G	Cys	Cys	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P97314 DOUBLE LIM PROTEIN-1 - MUS MUSCULUS (MOUSE), 193 aa.	2.90E-110	12
599	cg43986282	815	CGGTCTCTCCCA CAGCCCCCACA CTT[G/A]TTTCCA CCTCCCCAGAC AGGCATTTC	G	A	Asn	Asn	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P97314 DOUBLE LIM PROTEIN-1 - MUS MUSCULUS (MOUSE), 193 aa.	2.90E-110	12
600	cg42723058	651	GTCCCCCTACCA CCACCGGTCAC AGA[T/C]GTGAG CCTTGAGTTGCA GCAGCTGC	T	C	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:BAA82158 HCR PROTEIN - HOMO SAPIENS (HUMAN), 756 aa.	1.70E-107	
601	cg42723058	673	AGATGTGAGCC TTGAGTTGCAG CAG[C/T]TGCGG GAAGAACGGAA CCGCCTGGA	C	T	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:BAA82158 HCR PROTEIN - HOMO SAPIENS (HUMAN), 756 aa.	1.70E-107	

609	cg42028329	722	GCAAGGTTTCGC GATGTACGTATC ATC/TTCAGATC GGAACCTCACGT CGTCTA	C	T	Ile	Ile	SILENT- CODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q14499 SPLICING FACTOR - HOMO SAPIENS (HUMAN), 530 aa.	7.90E-101	14
610	cg42539705	165	AAACGGAACATAT TTCCAGATGAG GC/GA/GGGGTG CTGGAGGGGC TGTGGGTG	G	A	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75229 R31449_3 - HOMO SAPIENS (HUMAN), 813 aa (fragment).	1.20E-100	
611	cg42028329	115	CAAAGGAGAAC CCGTGCAGAAA ATT/C/T/CAGGC CAACATCTTCAA CAAGAGCA	C	T	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:P97434 P116RIP - MUS MUSCULUS (MOUSE), 1024 aa.	2.40E-99	
612	cg42028329	277	ACTTTGACAACC CAGTACACCGG TC/T/A/CGGAAA TGGCAGCGACG GTTCTTCA	T	A	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:P97434 P116RIP - MUS MUSCULUS (MOUSE), 1024 aa.	2.40E-99	
613	cg42028329	295	ACCGGTCTCGG AAATGGCAGCG ACG/G/A/TTCCT CATCCTTTACGA GCACGGCC	G	A	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:P97434 P116RIP - MUS MUSCULUS (MOUSE), 1024 aa.	2.40E-99	
614	cg42028329	310	GGCAGCGACGG TTCTTCATCCTT TA/C/T/GAGCAC GGCCTCTTGGC CTACGCC	C	T	Tyr	Tyr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:P97434 P116RIP - MUS MUSCULUS (MOUSE), 1024 aa.	2.40E-99	
615	cg42028329	316	GACGGTCTTCA TCCTTTACGAGC A/C/T/GGCCTCT TGCCTACGCC CTGGATG	C	T	His	His	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:P97434 P116RIP - MUS MUSCULUS (MOUSE), 1024 aa.	2.40E-99	

616	cg42028329	328	TCCTTACGAGC ACGGCCTCTTG CG[C/A]TACGCC CTGGATGAGAT GCCACGA	C	A	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:P97434 P116RIP - MUS MUSCULUS (MOUSE), 1024 aa.	2.40E-99	
617	cg42028329	352	GCTACGCCCTG GATGAGATGCC CAC[G/C]ACCCCT TCCTCAGGGCA CCATCAACA	G	C	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:P97434 P116RIP - MUS MUSCULUS (MOUSE), 1024 aa.	2.40E-99	
618	cg42392719	540	TCGCGAGAACG GCCTCAGTGCC AAG[G/T]CCCTT ACCCCTGCAGC TGGGCTCTG	G	T	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:CAB43370 HYPOTHETICAL 23.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 206 aa.	6.40E-99	
619	cg42392719	606	TCTCCCCCAAG GTGGGGTCTTC TAG[A/G]TCTGT GAGGAAGAGGT TCACATCTC	A	G	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:CAB43370 HYPOTHETICAL 23.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 206 aa.	6.40E-99	
620	cg42392719	627	CTAGATCTGTGA GGAAGAGGTTT AC[A/G]TCTCCC ACCATGCAGCT CTCTTCAG	A	G	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:CAB43370 HYPOTHETICAL 23.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 206 aa.	6.40E-99	
621	cg39512856	597	ACGGTCCGCCG GAAGCCACGTC ATA[G/A]ACGGT TTTACCCCGATG GTCTTCAA	G	A	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P03740 HYPOTHETICAL PROTEIN ORF194 - Bacteriophage lambda, 194 aa.	1.20E-98	
622	cg39512856	615	CGTCATAGACG GTTTACCCCGA TG[G/A]TCTTCAA CGAGATGCCAC GATGCCT	G	A	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P03740 HYPOTHETICAL PROTEIN ORF194 - Bacteriophage lambda, 194 aa.	1.20E-98	

623	cg39512856	663	CCTCATCACTGT TGAAACAGCC AC[A/G]AAGCCA GCCGGAATATC TGGCGGTG	A	G	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P03740 HYPOTHETICAL PROTEIN ORF194 - Bacteriophage lambda, 194 aa.	1.20E-98	
624	cg39512856	690	AGCCAGCCGGA ATATCTGGCGG TGC[A/G]ATATC GGTACTGTTTGC AGGCAGAC	A	G	Ile	Ile	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P03740 HYPOTHETICAL PROTEIN ORF194 - Bacteriophage lambda, 194 aa.	1.20E-98	
625	cg39512856	708	GCGGTGCAATA TCGGTACTGTTT GC[A/T]GGCAGA CCGGTATGAGG CGGAATAT	A	T	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P03740 HYPOTHETICAL PROTEIN ORF194 - Bacteriophage lambda, 194 aa.	1.20E-98	
626	cg39512856	717	TATCGGTACTGT TTGCAGGCAGA CC[G/T]GTATGA GGCGGAATATA TGCGTAC	G	T	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P03740 HYPOTHETICAL PROTEIN ORF194 - Bacteriophage lambda, 194 aa.	1.20E-98	
627	cg37445474	599	CCCTGCAAGCT CTGTATGGAAC GAT[C/T]CCCCA GATCTTTGGGA AGGAGAAT	C	T	Ile	Ile	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q63615 VACUOLAR PROTEIN SORTING HOMOLOG R-VPS33A - RATTUS NORVEGICUS (RAT), 597 aa.	2.80E-96	
628	cg30791729	294	CAGATCCAGTG GCCTTCCCCCA GCT[G/T]TGTC ACTGTGTCCAG GCTGTGGCT	G	T	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P12346 SEROTRANSFERRIN PRECURSOR (SIDEROPHILIN) (BETA-1-METAL BINDING GLOBULIN) - Rattus norvegicus (Rat), 698 aa.	3.20E-95	
629	cg42522690	454	GTGAACAGTGT AAATCAGTTTTT CA[T/C]TGGGAC ATGAAATCCAAG GATAAGG	T	C	His	His	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O35884 NEBULIN-RELATED ANCHORING PROTEIN (N-RAP) - MUS MUSCULUS (MOUSE), 1175 aa.	3.30E-94	10

630	cg42522690	625	CTCGAAAAGTCTCT TTGGTGAGGAA TA[T/C]ACAGAA GACTATGAGCA ACCCAGGG	T	C	Tyr	Tyr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O35884 NEBULIN-RELATED ANCHORING PROTEIN (N-RAP) - MUS MUSCULUS (MOUSE), 1175 aa.	3.30E-94	10
631	cg43982164	561	AGGTCACGTG TTGAAGCGTCCT CA[T/C]GTGGAT GAGTTCCTGCA GCCAATGG	T	C	His	His	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O15194 HYA22 - HOMO SAPIENS (HUMAN), 340 aa.	1.00E-90	
632	cg43980889	755	AAGACCATTTAC AAGTAGAAAATG A[T/C]GCTTACC CTGGTACCGAT AGAACAG	T	C	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O00581 HYPOTHETICAL 20.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 176 aa.	4.50E-89	
633	cg43980889	770	TAGAAAATGATG CTTACCCCTGGTA C[C/T]GATAGAA CAGAAAATGTTA AATATA	C	T	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O00581 HYPOTHETICAL 20.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 176 aa.	4.50E-89	
634	cg43980889	776	ATGATGCTTACC CTGGTACCGAT AG[A/G]ACAGAA AATGTTAAATAT AGACAAG	A	G	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O00581 HYPOTHETICAL 20.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 176 aa.	4.50E-89	
635	cg43980889	791	GTACCGATAGA ACAGAAAATGTT AA[A/G]TATAGA CAAAGTGGACCA TTTTGCCT	A	G	Lys	Lys	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O00581 HYPOTHETICAL 20.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 176 aa.	4.50E-89	
636	cg43955651	449	CTTCCACCCAG CCTGTGTTCTG GGC[G/A]CTGAC AAGGCCACCT TGTTGGTGT	G	A	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:AAD27745 CGI- 36 PROTEIN - HOMO SAPIENS (HUMAN), 165 aa.	1.10E-87	

637	cg43955651	476	TGACAAAGGCC ACCTTGTTGGTG TC[G/A]GGCTTG AGCGGAATGAA GCCACACT	G	A	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:AAD27745 CGI- 36 PROTEIN - HOMO SAPIENS (HUMAN), 165 aa.	1.10E-87	2
638	cg42353267	1516	GGCCTTCGATC CAGTCCATGAG CAA[T/C]GCCAT ATAGCGCGGCG CAGAGAGCT	T	C	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75249 R26660_1, PARTIAL CDS - HOMO SAPIENS (HUMAN), 291 aa (fragment).	2.60E-86	
639	cg37027086	258	GGGTTCTTCAAC TGGACACGGAG GCTT/CITCTACC CACCAGGCCCA AAACGAGG	T	C	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:BAA76824 KIAA0980 PROTEIN - HOMO SAPIENS (HUMAN), 1406 aa (fragment).	1.20E-83	
640	cg42688841	449	TCAACATAAGGT AGAAATTCATTA A[C/T]CTCAAGA AGCGAGCGTCA TAGTATA	C	T	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:Q02380 NADH-UBIQUINONE OXIDOREDUCTASE SGD SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-SGDH) (CI-SGDH) - Bos taurus (Bovine), 189 aa.	1.90E-83	
641	cg42688841	454	ATAAGGTAGAAT TTCATTAACTC A[A/G]GAAGCGA GCGTCATAGTAT AAAGAA	A	G	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:Q02380 NADH-UBIQUINONE OXIDOREDUCTASE SGD SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-SGDH) (CI-SGDH) - Bos taurus (Bovine), 189 aa.	1.90E-83	
642	cg42688841	461	AGAATTTTCAATTA ACCTCAAGAAG CG[A/G]GCGTCA TAGTATAAAGAA GGCTTGA	A	G	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:Q02380 NADH-UBIQUINONE OXIDOREDUCTASE SGD SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-SGDH) (CI-SGDH) - Bos taurus (Bovine), 189 aa.	1.90E-83	

[illegible]

643	cg42688841	476	TCAAGAAGCGA GCGTCATAGTAT AAAGGAAAGGC TTGACGACAAAC AGTCTCT	A	G	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:Q02380 NADH-UBIQUINONE OXIDOREDUCTASE SGD SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-SGDH) (CI-SGDH) - Bos taurus (Bovine), 189 aa.	1.90E-83	
644	cg43982291	1590	CACTGTGACCAT TTTGTACAGCAA GACAGACAGCG GTATATCCCAT CCAAAT	A	C	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q28282 C3VS PROTEIN - CANIS FAMILIARIS (DOG), 659 aa.	3.20E-79	
645	cg43982291	1716	GTAAGCTGTTT TCCCAGAGCTG TCG/AJACACTTT CGGCTGGGCAT TTAGACT	G	A	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q28282 C3VS PROTEIN - CANIS FAMILIARIS (DOG), 659 aa.	3.20E-79	
646	cg44003673	320	CATGCTTGGTG CCTGGTGCCAG GTGA/GJGTGAT GACGACCTCCA CGGCCTGCA	A	G	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:AAD25021 CALCIUM-REGULATED HEAT STABLE PROTEIN CRHSP-24 - HOMO SAPIENS (HUMAN), 147 aa.	1.60E-77	
647	cg44003673	449	CATCAGAGATGT GCAGGAAGATG TC[G/A]GGGCCG CCATCAGCTGG GGTAATGA	G	A	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:AAD25021 CALCIUM-REGULATED HEAT STABLE PROTEIN CRHSP-24 - HOMO SAPIENS (HUMAN), 147 aa.	1.60E-77	
648	cg44003673	470	TGTCGGGGCCG CCATCAGCTGG GGT[A/G]ATGAA GCCATGGCCCT TGGACCGGC	A	G	Ile	Ile	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:AAD25021 CALCIUM-REGULATED HEAT STABLE PROTEIN CRHSP-24 - HOMO SAPIENS (HUMAN), 147 aa.	1.60E-77	
649	cg44936941	1207	CGCGCACCTCG TCGCCGATCTG CTGT/CJCCGGT CTCCTTGCCGA GGAAGTCGT	T	C	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q62630 SM-20 - RATTUS NORVEGICUS (RAT), 355 aa.	7.00E-77	1

650	cg39523553	704	GGTCTGCCCCA TCCGGGATGGC TGC[C/A]GGTGG GTGATCGACGG TAGGCCGGA	C	A	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:CAB40855 PUTATIVE ADENINE GLYCOSYLASE - STREPTOMYCES COELICOLOR, 308 aa.	7.20E-75	
651	cg39523553	721	ATGGCTGCCGG TGGGTGATCGA CGG[T/C]AGGCC GGACAAATGCCC CGGCCCCGTC	T	C	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:CAB40855 PUTATIVE ADENINE GLYCOSYLASE - STREPTOMYCES COELICOLOR, 308 aa.	7.2E-75	
652	cg39523553	772	GAGACAGCCA TGGAAGGGCAC GGA[T/C]CGCCA GTGCCGGGGCG TGATTATGG	T	C	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:CAB40855 PUTATIVE ADENINE GLYCOSYLASE - STREPTOMYCES COELICOLOR, 308 aa.	7.2E-75	
653	cg39523553	823	ACGTGGTGCCG AACAGCCCTCA CGG[A/G]GTAA GGTCCAGATGG CTCTTTCCG	A	G	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:CAB40855 PUTATIVE ADENINE GLYCOSYLASE - STREPTOMYCES COELICOLOR, 308 aa.	7.2E-75	
654	cg39523553	874	CCTGGCCCCGAG CTCGATCAGGC ATC[A/G]AGGTG CCTGGAATCCTT ACTCGATG	A	G	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:CAB40855 PUTATIVE ADENINE GLYCOSYLASE - STREPTOMYCES COELICOLOR, 308 aa.	7.2E-75	
655	cg39523553	886	TCGATCAGGCA TCAAGGTGCCT GGA[A/G]TCCTT ACTCGATGACG GTTTAGTGC	A	G	Glu	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:CAB40855 PUTATIVE ADENINE GLYCOSYLASE - STREPTOMYCES COELICOLOR, 308 aa.	7.2E-75	

656	cg36728314	399	GCTGCTGCTTCT TCCTTGCGCAA C[G/A]ATCTTCT GGCAACGTCC TGGAAGA	G	A	Ile	Ile	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:BAA83051 KIAA1099 PROTEIN - HOMO SAPIENS (HUMAN), 804 aa.	1.3E-73	
657	cg41677120	375	TTCAGTGCACAA ATGAGATGAATG T[G/T]AACATCC CACAGTTGGCA GACAGTT	G	T	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q13492 CALM (TYPE I CALM PROTEIN) - HOMO SAPIENS (HUMAN), 652 aa.	1.10E-71	11
658	cg44126579	655	AGGAGTATTTCAT CATCCCCAATG CC[G/A]TAGCCT TCATGATTGAGG AATTTCG	G	A	Tyr	Tyr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:P90839 F16A11.1 - CAENORHABDITIS ELEGANS, 673 aa.	1.10E-71	16
659	cg44126579	712	GAGTGGCCCG CCAATCTGCATG AC[G/A]CCAGAA GTGACCACTGTT ACTTCAT	G	A	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:P90839 F16A11.1 - CAENORHABDITIS ELEGANS, 673 aa.	1.10E-71	16
660	cg38925480	73	AGAATCTCACCA GCCTTGTTGGTG CT[G/A]CATTTG CATAACAACCG CATCCAGC	G	A	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75473 ORPHAN G PROTEIN- COUPLED RECEPTOR HG38 - HOMO SAPIENS (HUMAN), 907 aa.	4.90E-69	
661	cg43323149	544	GCACCAGCGGA AGCCCTACAGA CGG[A/G]CTCAG CGTCATGCAAG GGCCCTACA	A	G	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P50636 GAMETOGENESIS EXPRESSED PROTEIN GEG-154 - Mus musculus (Mouse), 429 aa.	1.00E-68	1
662	cg43323149	559	CTACAGACGGA CTCAGCGTCAT GCA[A/G]GGGCC CTACAGCGAAA CAGCCAGCT	A	G	Gln	Gln	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P50636 GAMETOGENESIS EXPRESSED PROTEIN GEG-154 - Mus musculus (Mouse), 429 aa.	1.00E-68	1

663	cg43323149	664	GAAAATACAGC CGGTTAGAGTT CA[AG]GCCGAT GTCCAAAAGGA AATTTTCC	A	G	Gln	Gln	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P50636 GAMETOGENESIS EXPRESSED PROTEIN GEG-154 - Mus musculus (Mouse), 429 aa.	1.00E-68	1
664	cg34243633	263	CCACACACAGAG ATAATGCAGGC CAG[G/C]GAGGA GATTGCACCTGG ATGTCACCA	G	C	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O88552 CLAUDIN-2 - MUS MUSCULUS (MOUSE), 230 aa.	1.3E-68	
665	cg34243633	431	CAACTGCTGTCA CAATGCTGGCA CC[G/A]ACATAA GAACCTGTTTTG CAGCTGG	G	A	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O88552 CLAUDIN-2 - MUS MUSCULUS (MOUSE), 230 aa.	1.3E-68	
666	cg34243633	482	GGAGCAGCATG GCAACCAAGTG GCC[C/T]AAAAG CCCCAGAAGGC CTAGGATGT	C	T	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O88552 CLAUDIN-2 - MUS MUSCULUS (MOUSE), 230 aa.	1.3E-68	
667	cg43942922	231	AGCCACATCT CAGGCCACTAG GGG[C/A]AGAAC AAATAGGTCCTC TGTCAGA	C	A	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q14676 KIAA0170 PROTEIN - HOMO SAPIENS (HUMAN), 2089 aa.	2.3E-68	
668	cg43942922	291	CAGTTGTCCCC ACAGCCCCTGA GCT[C/T]CAGCC TTCCACCTCCAC AGACCAGC	C	T	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q14676 KIAA0170 PROTEIN - HOMO SAPIENS (HUMAN), 2089 aa.	2.3E-68	

669	cg43942922	396	CTGTCAAGACC CCTGAAACAGTT GT[G/C]CCACACA GCCCTGAGCT CCAGCCTT	G	C	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q14676 KIAA0170 PROTEIN - HOMO SAPIENS (HUMAN), 2089 aa.	2.3E-68	
670	cg43955219	1090	CCTGGCCAACA TGCCAAAACCC CGT[C/T]TCTACT AAAAATACAAAA AGCCGGG	C	T	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39194 !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! - Homo sapiens (Human), 593 aa.	6.4E-68	
671	cg29142822	401	CACTCACAAAA GGCAAGAAGC GC[A/G]AGGAGG GATAATGTCTTG GAAGCCA	A	G	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q07320 ZEIN-ALPHA PRECURSOR (ZSF4C4) - ZEA MAYS (MAIZE), 266 aa.	2.5E-65	
672	cg43988710	397	TTGGTGAAGAG GTTGTACAGCA CTC[G/T]TAGTG TAGACTTCAGGT CACAGTTG	G	T	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:AAD34051 CGI- 56 PROTEIN - HOMO SAPIENS (HUMAN), 317 aa.	1.4E-62	
673	cg43988710	404	AGAGGTTGTAC AGCACTCGTAG TGT[A/G]GACTT CAGGTCACAGT TGACAATGT	A	G	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:AAD34051 CGI- 56 PROTEIN - HOMO SAPIENS (HUMAN), 317 aa.	1.4E-62	
674	cg39516123	1049	GCTTGGACCGG CATGTGGCCTAT GGT[C/G]GGCTAT TCTACCCCGGA GGATCGGA	T	C	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q04205 TENSIN - Gallus gallus (Chicken), 1744 aa.	5.1E-62	
675	cg39516123	452	CAGGCAGCCTG GGACAGCCCGAG CCC[G/A]TCTGC CCAGAGAAACT ACCAGAGCT	G	A	Pro	Pro	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q04205 TENSIN - Gallus gallus (Chicken), 1744 aa.	5.1E-62	

676	cg39516123	563	TCAGCTCTCTCTC CGGAAAGCCAG GC[C/T]CGAGCT CAGTTCAGTGT GGCTGGCG	C	T	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q04205 TENSIN - Gallus gallus (Chicken), 1744 aa.	5.1E-62	
677	cg39516123	620	CGGTGCCTGGG AGCCCTCAGGC GCG[C/T]CACAG AACAGTGGCA CCAACACTC	C	T	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q04205 TENSIN - Gallus gallus (Chicken), 1744 aa.	5.1E-62	
678	cg42731307	435	GGAAATGAGCC AAAGTTCGCATG AA[T/C]CCACGG AAGTTTACCTGG TCCTCTC	T	C	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q99653 CALCIUM-BINDING PROTEIN P22 (CALCIUM-BINDING PROTEIN CHP) - Homo sapiens (Human), 194 aa.	2.6E-61	
679	cg44128084	440	CCGGACAACAC CGTTGGAGTTCT TT[T/C]GCCGTC AACGAGTTGTCT CTGGAAA	T	C	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O33196 HYPOTHETICAL 32.9 KD PROTEIN - MYCOBACTERIUM TUBERCULOSIS, 307 aa.	1.70E-59	
680	cg44128084	665	TGAGCGCTCAC GCTCTCTTTGCT CG[A/G]CCGCTG GTCATGAGCCC AGCTGCTC	A	G	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O33196 HYPOTHETICAL 32.9 KD PROTEIN - MYCOBACTERIUM TUBERCULOSIS, 307 aa.	1.70E-59	
681	cg44128084	680	TCTTTGCTCGAC CGCTGGTCATG AG[C/T]CCAGCT GCTCGAGTGGA CCTTGACA	C	T	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O33196 HYPOTHETICAL 32.9 KD PROTEIN - MYCOBACTERIUM TUBERCULOSIS, 307 aa.	1.70E-59	
682	cg44128084	695	TGGTCATGAGC CCAGCTGCTCG AGT[G/A]GACCT TGACATCCAGC CAGACGGTT	G	A	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O33196 HYPOTHETICAL 32.9 KD PROTEIN - MYCOBACTERIUM TUBERCULOSIS, 307 aa.	1.70E-59	

683	cg44128084	728	ACATCCAGCCA GACGGTTCAGA ATC[A/G]GCGGT TCTGTGGTGCG ACGGGCGCC	A	G	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O33196 HYPOTHETICAL 32.9 KD PROTEIN - MYCOBACTERIUM TUBERCULOSIS, 307 aa.	1.70E-59	
684	cg30455661	289	CCACATACACAA CAGCATATACCT T[C/T]CCTGGGA TTCTCAAGTGGT TTGAAG	C	T	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q14185 DOCK180 PROTEIN - HOMO SAPIENS (HUMAN), 1865 aa.	5.20E-58	
685	cg30455661	347	GATTTCAACAGA AGAAATCAGCC CT[C/T]TGGAGA ATGCCATAGAAA CCATGGA	C	T	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q14185 DOCK180 PROTEIN - HOMO SAPIENS (HUMAN), 1865 aa.	5.20E-58	
686	cg30455661	382	CCATAGAAACCA TGGAGCTGACC AA[C/T]GAGAGG ATCAGCAACTGT GTTGAGC	C	T	Asn	Asn	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q14185 DOCK180 PROTEIN - HOMO SAPIENS (HUMAN), 1865 aa.	5.20E-58	
687	cg43302460	827	AGCTCGGGAGT ACAGGTGAAAC TTC[T/G]CGAATT GCCTGTTCCCTC TTTCTGA	T	G	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:CAB43289 HYPOTHETICAL 12.7 KD PROTEIN - HOMO SAPIENS (HUMAN), 116 aa (fragment).	1.70E-57	2
688	cg43153425	101	AAGCCCGACTT TCTGTAGGAAGT AA[C/T]CGTGAC CGAGAGATCAG CATGTCCTG	C	T	Asn	Asn	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:BAA83061 KIAA1109 PROTEIN - HOMO SAPIENS (HUMAN), 1957 aa (fragment).	2.40E-57	
689	cg43153425	107	GACTTCTGTAG GAAGTAACCGT GA[C/T]CGAGAG ATCAGCATGTCT GTCGGTC	C	T	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:BAA83061 KIAA1109 PROTEIN - HOMO SAPIENS (HUMAN), 1957 aa (fragment).	2.40E-57	

690	cg43153425	128	GTGACCGAGAG ATCAGCATGTCT GT[C/T]GGTCTG GGAAGGTCACA GTTAGACT	C	T	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:BAA83061 KIAA1109 PROTEIN - HOMO SAPIENS (HUMAN), 1957 aa (fragment).	2.40E-57	
691	cg43153425	140	TCAGCATGTCTG TCGGTCTGGGA AG[G/A]TCACAG TTAGACTCCAAA GGAGGAG	G	A	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:BAA83061 KIAA1109 PROTEIN - HOMO SAPIENS (HUMAN), 1957 aa (fragment).	2.40E-57	
692	cg43153425	146	TGCTCTCGGT CTGGGAAGGTC ACA[G/A]TTAGA CTCCAAAGGAG GAGTAGTTG	G	A	Gln	Gln	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:BAA83061 KIAA1109 PROTEIN - HOMO SAPIENS (HUMAN), 1957 aa (fragment).	2.40E-57	
693	cg43153425	152	TCGGTCTGGGA AGGTCACAGTTA GA[C/T]TCCAAA GGAGGAGTAGT TGGTGGGA	C	T	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:BAA83061 KIAA1109 PROTEIN - HOMO SAPIENS (HUMAN), 1957 aa (fragment).	2.40E-57	
694	cg43153425	155	GTCTGGGAAGG TCACAGTTAGAC TC[C/T]AAAGGA GGAGTAGTTGG TGGGACCA	C	T	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:BAA83061 KIAA1109 PROTEIN - HOMO SAPIENS (HUMAN), 1957 aa (fragment).	2.40E-57	
695	cg43153425	251	CAAATCAGCAAC CAAAACCACAAA T[A/T]CAAAATTAC TATGGGTTCTAC TGAAT	A	T	Ile	Ile	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:BAA83061 KIAA1109 PROTEIN - HOMO SAPIENS (HUMAN), 1957 aa (fragment).	2.40E-57	
696	cg43153425	287	TGGGTTCTACTG AATCTCGGGTT GA[C/T]TACATG GGCTCAAGCAT CCTCATGG	C	T	Asp	Asp	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:BAA83061 KIAA1109 PROTEIN - HOMO SAPIENS (HUMAN), 1957 aa (fragment).	2.40E-57	

[illegible]

703	cg44015614	1379	AGGGCATTGCG AGAAACTGGCC CTT[A/G]ATAAG GAAATCAAACATC CACATGTT	A	G	Ile	Ile	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P91343 HYPOTHETICAL 49.0 KD TRP-ASP REPEATS CONTAINING PROTEIN F55F8.5 IN CHROMOSOME I - Caenorhabditis elegans, 439 aa.	3.30E-54	
704	cg42380652	406	AGTCCAGGCAG GGGCCCCACGTC CTC[T/C]CGGTA CACCCCTTCCAG GAAGGGGC	T	C	Arg	Arg	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q62739 RABIN3 - RATTUS NORVEGICUS (RAT), 460 aa.	4.20E-54	
705	cg43931038	425	TCCTCTCTAGAG TCCCGCGGCTC AC[A/G]GCCTT GCTCGAAGGG CAACTTGT	A	G	Ala	Ala	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O46082 EG:63B12.2 PROTEIN - DROSOPHILA MELANOGASTER (FRUIT FLY), 254 aa.	6.10E-54	
706	cg43931038	436	GTCCCGCGGCT CACAGCCTTTG CTG[C/G]GAAGG GCAACTTGTGG GCAACCTGG	C	G	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O46082 EG:63B12.2 PROTEIN - DROSOPHILA MELANOGASTER (FRUIT FLY), 254 aa.	6.10E-54	
707	cg43931038	463	AAGGGCAACTT GTGGGCAACCT GGT[C/T]AAGGA AACCTTGACTTC TTCAAAAT	C	T	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O46082 EG:63B12.2 PROTEIN - DROSOPHILA MELANOGASTER (FRUIT FLY), 254 aa.	6.10E-54	
708	cg43931038	469	AACTTGTGGGC AACCTGGTCAA GGA[A/C]ACCTT GACTTCTTCAAA TTCACAAC	A	C	Val	Val	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O46082 EG:63B12.2 PROTEIN - DROSOPHILA MELANOGASTER (FRUIT FLY), 254 aa.	6.10E-54	
709	cg43931038	478	GCAACCTGGTC AAGGAAACCTT GAC[T/C]TCTCA AATTCACAACGC CCACCCA	T	C	Glu	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O46082 EG:63B12.2 PROTEIN - DROSOPHILA MELANOGASTER (FRUIT FLY), 254 aa.	6.10E-54	

710	cg43931038	496	CCTTGACTTCTT CAAAATTCACAAC G[C/T]CCACCCA TCTCTACAACAA GGCGGC	C	T	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O46082 EG:63B12.2 PROTEIN - DROSOPHILA MELANOGASTER (FRUIT FLY), 254 aa.	6.10E-54	11
711	cg43931038	562	TCACGTAGTGG TCAATAGCACCT TT[G/A]CCTCCC CCCATGGGATG CCCAACAC	G	A	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O46082 EG:63B12.2 PROTEIN - DROSOPHILA MELANOGASTER (FRUIT FLY), 254 aa.	6.10E-54	11
712	cg43338979	360	CATCATCTCTG AAGATGCTAGC AC[C/T]GTTCTT GTTATATTCCAA CTCACTC	C	T	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O45933 Y43F4B.4 - CAENORHABDITIS ELEGANS, 363 aa.	1.40E-53	18
713	cg38450437	104	GAATTGGTTCTG AGGAGTTTGAG GA[G/A]CTTCTTT TACTGATGGACA GAAATC	G	A	Glu	Glu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O43168 KIAA0443 - HOMO SAPIENS (HUMAN), 1395 aa.	3.50E-52	
714	cg38450437	47	CCAGGGAAAGT GCACAGCCAGA GAA[T/C]TGGTC TTGCAACTGCAT CCAGTGTG	T	C	Asn	Asn	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O43168 KIAA0443 - HOMO SAPIENS (HUMAN), 1395 aa.	3.50E-52	
715	cg43314946	458	CCTTCCGGATG ACTTTCTCCGCA TC[C/T]TGCCCC AGCAGCTGGAC AGCATACA	C	T	Leu	Leu	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:AAD37447 BAW - FUGU RUBRIPES (JAPANESE PUFFERFISH) (TAKIFUGU RUBRIPES), 402 aa.	1.60E-51	17
716	cg44010070	320	TCAAGCACTCG GACGGGACGCG CAC[T/C]TGCGC CAAGCTCTATGA CAAGAGCG	T	C	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:O35775 SYNCOLLIN (SIP9) - Rattus norvegicus (Rat), 145 aa.	6.40E-51	

717	cg39380052	563	ACCTCATCACCC CGTACCATCAG AC[C/T]CTCGAC AAGTCACTGA GCGTTTTTC	C	T	Thr	Thr	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:CAB42016 PUTATIVE ADENYLOSUCCINATE SYNTHETASE - STREPTOMYCES COELICOLOR, 427 aa.	1.30E-50	
718	cg39380052	641	GTCGTGGCATC GGCCCGACCTA CTC[T/C]GACAA GATCAATCGGAT GGGTATTC	T	C	Ser	Ser	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:CAB42016 PUTATIVE ADENYLOSUCCINATE SYNTHETASE - STREPTOMYCES COELICOLOR, 427 aa.	1.30E-50	
719	cg39380052	662	ACTCTGACAAGA TCAATCGGATG GGT[C/G]ATTGCG GTCCAGGATCTT TTCGACG	T	C	Gly	Gly	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:CAB42016 PUTATIVE ADENYLOSUCCINATE SYNTHETASE - STREPTOMYCES COELICOLOR, 427 aa.	1.30E-50	
720	cg43298242	585	TCATCGACAACC AGAACCTCCTCT TTT/C]GAGCTCT CCTACAAGCTG GAGGCAA	T	C	Phe	Phe	SILENT- CODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q92565 MYELOBLAST KIAA0277 - HOMO SAPIENS (HUMAN), 580 aa.	1.40E-50	
721	cg43298242	138	CTGAAGATCTGT TGGCAGGGCTC AC[A/G]GAGACG GGGGTGAGGGG AGAGATCG	A	G	Ser	Ser	SILENT- CODING	water_ch annel	Human Gene SWISSPROT- ID:O14520 AQUAPORIN-7 LIKE (AQUAPORIN ADIPOSE) (AQPAP) - HOMO SAPIENS (HUMAN), 342 aa.	1.30E-163	
722	cg43298242	150	TGGCAGGGCTC ACAGAGACGGG GGT[G/A]AGGGG AGAGATCGTGG GTTTCATGAG	G	A	Leu	Leu	SILENT- CODING	water_ch annel	Human Gene SWISSPROT- ID:O14520 AQUAPORIN-7 LIKE (AQUAPORIN ADIPOSE) (AQPAP) - HOMO SAPIENS (HUMAN), 342 aa.	1.30E-163	

723	cg43970780	1501	GGAGTTCCTGGT TCTGGTAGATG GAA[G/A]CTTTCT CTTCAACAGGT CCAGACA	G	A	Ala	Val (1096)	CONSERVATI VE	apoptosi s	Human Gene SWISSNEW-ID:Q92785 ZINC-FINGER PROTEIN UBI-D4 (APOPTOSIS RESPONSE ZINC FINGER PROTEIN REQUIEM) - HOMO SAPIENS (HUMAN), 391 aa. pcls:SWISSPROT-ID:Q92785 ZINC-FINGER PROTEIN UBI-D4 (APOPTOSIS RESPONSE ZINC FINGER PROTEIN REQUIEM) - HOMO SAPIENS (HUMAN), 391 aa.	2.30E-212	11
724	cg43957906	460	GGAGTCCTTGG CGGGTCATAT GGG[T/C]GCTCC TTGAGGGGAT CTCCAGGAC	T	C	His	Arg (1097)	CONSERVATI VE	ATPase_ associat ed	Human Gene Similar to SWISSPROT- ID:Q16864 VACUOLAR ATP SYNTHASE SUBUNIT F (EC 3.6.1.34) (V-ATPASE F SUBUNIT) (V- ATPASE 14 KD SUBUNIT) - HOMO SAPIENS (HUMAN), 119 aa.	2.20E-58	12
725	cg43952088	2923	TGAGGGGAGCG TCGCCGGCCGC GGA[G/A]CAGAT GCCGCGGGGGC CGCTCGCAG	G	A	Ala	Val (1098)	CONSERVATI VE	cadherin	Human Gene SPTREMBL-ID:Q15065 OB-CADHERIN-1 - HOMO SAPIENS (HUMAN), 796 aa.	0.00E+00	16
726	cg43956666	613	ACTCCTGTTCTG GGGACAGTTTG GT[A/G]TTAAAC ACTTAAATATAG ATCCGG	A	G	Ile	Val (1099)	CONSERVATI VE	cadherin	Human Gene SWISSNEW-ID:Q08722 LEUKOCYTE SURFACE ANTIGEN CD47 PRECURSOR (ANTIGENIC SURFACE DETERMINANT PROTEIN OA3) (INTEGRIN ASSOCIATED PROTEIN) (IAP) (MER6) - HOMO SAPIENS (HUMAN), 323 aa. pcls:SWISSPROT-ID:Q08722 LEUKOCYTE SURFACE ANTIGEN CD47 PRECURSOR (ANTIGENIC SURFACE DETERMINANT PROTEIN OA3) (INTEGRIN ASSOCIATED PROTEIN) (IAP) (MER6) - HOMO SAPIENS (HUMAN), 323 aa.	1.20E-167 (3q13.1)	3

727	cg43942011	1327	TTCCCCATGTGA AACATCTGGCTT G[C/T]GACAGGT GATTTTTCACA GGTAGG	C	T	Arg	His (1100)	CONSERVATI VE	complem entrecept	Human Gene Similar to TREMBLNEW-ID:E246058 COMPLEMENT RECEPTOR 2 - MUS MUSCULUS (MOUSE), 651 aa (fragment).	1.10E-69	1 (1q32)
728	cg43973728	987	TATGAACACCCC AGATCTGAAGAA G[T/C]TGCTGTT CTGAAACAGAA GTTGGAG	T	C	Val	Ala (1101)	CONSERVATI VE	cyclin	Human Gene SWISSPROT- ID:P51946 CYCLIN H (MO15- ASSOCIATED PROTEIN) (P37) (P34) - HOMO SAPIENS (HUMAN), 323 aa.	2.60E-172	5 (5q13.3)
729	cg44017721	291	TCCTGCTCCTCC GTGGCCTCCTTT G[G/A]CAGCGCT GGCCAAAGCCCC GGGTGAG	G	A	Ala	Val (1102)	CONSERVATI VE	cytochro me	Human Gene Similar to SPTREMBL- ID:O00761 CYTOCHROME OXIDASE SUBUNIT VIA HEART ISOFORM PRECURSOR (EC 1.9.3.1) (CYTOCHROME-C OXIDASE) (CYTOCHROME A(3)) (CYTOCHROME AA(3)) - HOMO SAPIENS (HUMAN), 97 aa.	2.40E-52	22
730	cg43273880	5428	CAAAAGAAAGAA GACGACGTGAC TG[G/C]GGGTAA GAAACCATTTG TCCAGAG	G	C	Gly	Ala (1103)	CONSERVATI VE	dna_ma _bind	Human Gene SWISSPROT- ID:O14647 CHROMODOMAIN- HELICASE-DNA-BINDING PROTEIN 2 (CHD-2) - HOMO SAPIENS (HUMAN), 1739 aa.	0.00E+00	15
731	cg43992911	485	GAAGAAGAACTT TTTTAAACTGAA C[A/G]ATAAAAG TGAAAAAGATAA GAAGGA	A	G	Asn	Asp (1104)	CONSERVATI VE	glycoprot ein	Human Gene SWISSPROT- ID:P08183 MULTIDRUG RESISTANCE PROTEIN 1 (P- GLYCOPROTEIN 1) - HOMO SAPIENS (HUMAN), 1280 aa.	0.00E+00	7
732	cg41029366	890	TGCGGCCACAA AGAGGACGCGG GCG[T/C]GGTGT GCTCAGAGCAC CAGTCCTGG	T	C	Val	Ala (1105)	CONSERVATI VE	glycoprot ein	Human Gene SPTREMBL-ID:Q61003 T CELL SURFACE GLYCOPROTEIN CD6 - MUS MUSCULUS (MOUSE), 665 aa.	1.00E-234	11

733	cg43931167	2546	CGAGAACTGAA GAAAGCAAGAA CAGT/GJCCTAC AAATGGATGAAC TCAAATGT	T	G	Val	Gly (1106)	CONSERVATIVE	helicase	Human Gene SWISSPROT- ID:O14232 PUTATIVE HELICASE C6F12.16 IN CHROMOSOME I - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 1117 aa.	3.30E+07	5
734	cg43925670	2360	AATCTGAATTTT GTCATACTCTTC T[C/T]TCATTTT AAATTAAGTTTT AAATC	C	T	Arg	Lys (1107)	CONSERVATIVE	interferon	Human Gene SWISSPROT- ID:Q16666 GAMMA-INTERFERON- INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa.lpcds:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment).	0.00E+00	1
735	cg43925670	2474	TAGAACAATGTT CTTGATTTTTTT [C/G]CCATCTTTA CAGACATAAGT GAGCC	C	G	Gly	Ala (1108)	CONSERVATIVE	interferon	Human Gene SWISSPROT- ID:Q16666 GAMMA-INTERFERON- INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa.lpcds:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment).	0.00E+00	1

740	cg43105476	702	GCGAAACCCAGT TCGGTCTTTCAA AT[C/T]GGGATT AGCACCTCTAA GTAGCAGT	C	T	Asp	Asn (1113)	CONSERVATIVE	kinase inhibitor	Human Gene Similar to SWISSPROT-ID: P42773 CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) - HOMO SAPIENS (HUMAN), 168 aa.	7.80E-86	
741	cg38642684	290	ATATTGCCTAGT AATTTCTGATAA TTC/TATTTAAGG TATGTAAGTTGC TAGTA	C	T	Asp	Asn (1114)	CONSERVATIVE	nuclease	Human Gene Similar to SWISSPROT-ID: P10266 RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] - HOMO SAPIENS (HUMAN), 874 aa. pcds:SWISSPROT-ID: P10266 RETROVIRUS-RELATED POLYPROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) - HOMO SAPIENS (HUMAN), 874 aa.	2.60E-50	
742	cg39518465	864	CACCTTCCTAAAG GAGATGAAGGA AG[C/T]CCTGGG CACCCCTGGCG CAGCCAAAT	C	T	Ala	Val (1115)	CONSERVATIVE	oncogene	Human Gene SWISSPROT-ID: P15498 VAV PROTO-ONCOGENE - HOMO SAPIENS (HUMAN), 846 aa.	0.00E+00	
743	cg43021380	176	CAGCCGCCCGG GGGGCTGCAGC GCC[G/A]TTAGT GCCACACGGCTG TCTATTTGA	G	A	Val	Ile (1116)	CONSERVATIVE	phosphatase	Human Gene SWISSPROT-ID: Q16849 PROTEIN-TYROSINE PHOSPHATASE N PRECURSOR (EC 3.1.3.48) (R-PTP-N) (PTP IA-2) (ISLET CELL ANTIGEN 512) (ICA 512) (ISLET CELL AUTOANTIGEN 3) - HOMO SAPIENS (HUMAN), 979 aa.	0.00E+00	2
744	cg39728924	365	CAATTGTGGAG AAGAGTATTTT AT[G/A]TCGCTA CTCAAGGACCA CTGCTGAG	G	A	Val	Ile (1117)	CONSERVATIVE	phosphatase	Human Gene Similar to TREMBLNEW-ID: D1024666 PROTEIN-TYROSINE PHOSPHATASE (EC 3.1.3.48) - MUS MUSCULUS (MOUSE), 426 aa.	1.20E-64	

745	cg42710490	851	CAACCAGCCTAT TGGGGGAAGAA ATGATCCAGG GTGGAATCCGT TTTGGGGA	G	A	Val	Ile (1118)	CONSERVATI VE	polymera se	Human Gene SWISSNEW-ID:O54888 DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135) (RNA POLYMERASE I 127 KD SUBUNIT) - RATTUS NORVEGICUS (RAT), 1135 aa. pcis:TREMBLNEW-ID:G2739048 RNA POLYMERASE I 127 KDA SUBUNIT - RATTUS NORVEGICUS (RAT), 1135.aa.	8.90E-172	
746	cg44001078	316	GGTTATCAGGA ACTGGGATCTT CA[C/T]GGATT CCATCTTGTTCT TCATCCA	C	T	Arg	His (1119)	CONSERVATI VE	struct	Human Gene TREMBLNEW- ID:G2920823 CARDIAC MYOSIN BINDING PROTEIN-C - HOMO SAPIENS (HUMAN), 1274 aa.	0.00E+00	
747	cg43916919	1113	AGGTAGGAGTC CCCCGAGAAGA AGA[C/T]GCCCT GGTCTCTTGC GCCACAGGC	C	T	Val	Ile (1120)	CONSERVATI VE	struct	Human Gene SWISSNEW-ID:P40121 MACROPHAGE CAPPING PROTEIN (ACTIN-REGULATORY PROTEIN CAP-G) - HOMO SAPIENS (HUMAN), 348 aa. pcis:SWISSPROT-ID:P40121 MACROPHAGE CAPPING PROTEIN (ACTIN-REGULATORY PROTEIN CAP-G) - HOMO SAPIENS (HUMAN), 348 aa.	4.3E-188	2 (2cen)
748	cg42930605	463	CAGCTCCTTGCT GGTCTTCTGCA CC[C/T]TCACCT CCATGTCGTACT TCTCCTC	C	T	Arg	Lys (1121)	CONSERVATI VE	struct	Human Gene Similar to SWISSPROT- ID:P48788 TROPONIN I, FAST SKELETAL MUSCLE (TROPONIN I, FAST-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 181 aa.	1E-92	11 (11p15.5)
749	cg36824552	230	AAGACGAGCCG AGGCTTCACCTA CC[A/G]CCTGCA CTTCTGGCTCG GAAAGGAG	A	G	His	Arg (1122)	CONSERVATI VE	struct	Human Gene Similar to SWISSPROT- ID:Q28046 ADSEVERIN (SCINDERIN) (SC) - BOS TAURUS (BOVINE), 715 aa.	4E-80	

750	cg42522566	377	CAACATCATGAA CCAGCTCAGCC AC[G/A]TAAACTT GATCCAACTTTA TGATGC	G	A	Val	Ile (1123)	CONSERVATI VE	struct	Human Gene Similar to SWISSPROT- ID:P07313 MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (EC 2.7.1.117) (MLCK) - ORYCTOLAGUS CUNICULUS (RABBIT), 607 aa.	6E-55	
751	cg42522566	509	GTACCACCTCA CTGAGTTGGAT GTG[G/A]TCTTG TTCACGAGGCA GATCTGTGA	G	A	Val	Ile (1124)	CONSERVATI VE	struct	Human Gene Similar to SWISSPROT- ID:P07313 MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (EC 2.7.1.117) (MLCK) - ORYCTOLAGUS CUNICULUS (RABBIT), 607 aa.	6E-55	
752	cg42489842	481	TGCAAGTGAATA TGCCAAATACTG CT[A]CAGAAATA TTAGGAGTTGCA GCTAC	T	A	Ser	Thr (1125)	CONSERVATI VE	tm7	Human Gene Homologous to SWISSPROT-ID:Q02038 NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE) (MITOCHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP) (SOLUBLE ANGIOTENSIN- BINDING PROTEIN) (SABP) - SUS SCROFA (PIG), 704 aa.	7.3E-106	
753	cg43919398	2201	GTTAGTCTCTGT GGTGTCCTATA ATT[C]CATTTGG GGTCCAAACATTC ACATTT	T	C	Ile	Val (1126)	CONSERVATI VE	transcript factor	Human Gene SWISSPROT- ID:Q14188 TRANSCRIPTION FACTOR DP-2 (E2F DIMERIZATION PARTNER 2) - HOMO SAPIENS (HUMAN), 385 aa.	2.7E-202	3
754	cg20612302	300	ATGGAGGCGGC CCACATGGCGG CCA[C/G]CGCCA TCCTCAACCTGT CCACGCGC	C	G	Thr	Ser (1127)	CONSERVATI VE	transcript factor	Human Gene Similar to SPTREMBL- ID:O08996 MYELIN TRANSCRIPTION FACTOR 1-LIKE - MUS MUSCULUS (MOUSE), 1182 aa.	1.7E-53	
755	cg44928196	1474	GGCTCTGTTCC ATGGGAAATTCA TA[G/A]ACACGG GTTTTCTTTAC CATTCTA	G	A	Asp	Asn (1128)	CONSERVATI VE	ubiquitin	Human Gene TREMBLNEW- ID:G2827198 UBIQUITIN PROTEIN LIGASE - MUS MUSCULUS (MOUSE), 854 aa.	0	

756	cg43301812	3784	GGCTGGTCCCT CTCCATGGCTG GGAATC/GCTCT GCTGCGCTTGG TTTTGCCCG	T	C	His	Arg (1129)	CONSERVATI VE	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:Q93075 HYPOTHETICAL PROTEIN KIAA0218 - Homo sapiens (Human), 761 aa.	0.00E+00	3
757	cg43917191	2735	GCTTCTCTTTTC ACATTGTATGTA TTC/TTCAGGTGT TCTTGCAACTCC AAAAACA	C	T	Asp	Asn (1130)	CONSERVATI VE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA74849 KIAA0826 PROTEIN - HOMO SAPIENS (HUMAN), 1236 aa (fragment).	0.00E+00	4
758	cg43918356	2637	GCTCATGTCATC TTCATCTAGAAA C[G/A]CCCTCAC GAAATGGAATT GCTGCC	G	A	Ala	Val (1131)	CONSERVATI VE	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q75176 KIAA0692 PROTEIN - HOMO SAPIENS (HUMAN), 783 aa (fragment).	0.00E+00	12
759	cg43932090	1186	TCTTTTCAAGCT TCTTTATGTTG TTT/CJTATTGTCT TCATTTTCTTGA AGTTC	T	C	Lys	Arg (1132)	CONSERVATI VE	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O00566 M PHASE PHOSPHOPROTEIN 10 - HOMO SAPIENS (HUMAN), 672 aa (fragment).	0.00E+00	
760	cg43950437	794	AGCCAGAGGCT GGTACCTAGAA CCA[G/C]TGGAT GGTTCTTGGCT GATGGCGC	G	C	Thr	Ser (1133)	CONSERVATI VE	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q15021 ORF - HOMO SAPIENS (HUMAN), 1401 aa.	0.00E+00	12
761	cg42935995	743	GCCTCGCTCCC CGTCTGAGAGC CTC[A/G]CGCCC TCCAGCCAGCC GTCACCTGCT	A	G	Val	Ala (1134)	CONSERVATI VE	UNCLAS SIFIED	Human Gene SWISSNEW- ACC:Q12774 PROBABLE GUANINE NUCLEOTIDE REGULATORY PROTEIN TIM (ONCOGENE TIM) (P60 TIM) (TRANSFORMING IMMORTALIZED MAMMARY ONCOGENE) - Homo sapiens (Human), 519 aa.	1.00E-274	
762	cg43971614	2578	TCCATTGAATC CAATCCCCCAT GG[A/G]CATAAG AAGAGTCTTTC CATAAAA	A	G	Val	Ala (1135)	CONSERVATI VE	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q13283 GAP SH3 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 466 aa.	5.30E-253	5

763	cg43922856	1581	CTTGAAATTTC AGTCACCCTATT G[A/G]CAACTAA GGATTCGTTGCT TGAAGC	A	G	Val	Ala (1136)	CONSERVATI VE	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:P42167 THYMOPOIETINS BETA AND GAMMA (TP BETA AND TP GAMMA) - Homo sapiens (Human), 453 aa.	2.00E-237	12 (12q22)
764	cg43922856	1783	CCACTTGTCCAT TCAGTCTCAGTT A[T/C]TCCAGCTT GAGAATAGCTCT GATTG	T	C	Ile	Val (1137)	CONSERVATI VE	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:P42167 THYMOPOIETINS BETA AND GAMMA (TP BETA AND TP GAMMA) - Homo sapiens (Human), 453 aa.	2.00E-237	12 (12q22)
765	cg43955639	282	GGCCGCGGGG GGATAGCTGCC CAGG[C/G]TCAG GAGGCTCTTGG GCTCCTGCCA	C	G	Ser	Thr (1138)	CONSERVATI VE	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O15417 CAGL79 - HOMO SAPIENS (HUMAN), 413 aa (fragment).	2.80E-215	
766	cg41022625	1121	CACGGCGTTCT GGATCGTCTTCT CC[A/G]TCATTC ACATCATCGCCA CCCTGCT	A	G	Ile	Val (1139)	CONSERVATI VE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34036 CGI-40 PROTEIN - HOMO SAPIENS (HUMAN), 845 aa.	2.00E-207	11
767	cg43119894	1960	TGAGCATAGCT CTGAGCTCTCTT TA[C/T]ACGGTC AGGTCCACAT AATGCATT	C	T	Val	Ile (1140)	CONSERVATI VE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAA75235 LACTOSYLKERAMIDE ALPHA-2,3- SIALYLTRANSFERASE (EC 2.4.99.9) - MUS MUSCULUS (MOUSE), 387 aa.	2.30E-190	2
768	cg43303845	1109	AGAACGAGAGA GGCTGGAGAGA CTG[C/G]AACGG GAGAGGCAAGA AAGGGAGCG	C	G	Gln	Glu (1141)	CONSERVATI VE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O93263 AVENA - GALLUS GALLUS (CHICKEN), 550 aa.	1.90E-138	
769	cg44927166	531	GTCTTTGTCTTC CCAATCCCTTTG G[C/T]GTTCTCG TTCCTTATCCCT TTCTCT	C	T	Arg	His (1142)	CONSERVATI VE	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:BAA74876 KIAA0853 PROTEIN - HOMO SAPIENS (HUMAN), 967 aa (fragment).	3.70E-133	13

770	cg38059286	473	AGCTGTATAGCT CCAGTGGTCCT GA[G/T]CTCCGC CGCTCCCTCTTC TCACCTGA	G	T	Glu	Asp (1143)	CONSERVATIVE	UNCLASSIFIED	Human Gene Homologous to TREMBLIN-ACC:AAD39906 FH1/FH2 DOMAIN-CONTAINING PROTEIN FHOS - HOMO SAPIENS (HUMAN), 1164 aa.	4.00E-129	
771	cg29351416	333	CTGCCACAGCCA GCCCCATCCCC TGA[G/T]GACCT GGCTTTGTCAAT GGGCACCA	G	T	Glu	Asp (1144)	CONSERVATIVE	UNCLASSIFIED	Human Gene Homologous to SPTREMBL-ACC:Q03626 ALPHA-1- INHIBITOR III PRECURSOR, ISOFORM 2 (RAT PLASMA PROTEINASE INHIBITOR ALPHA-1- INHIBITOR III GROUP 3 VARIANT 36A) (ALPHA-1 PROTEINASE INHIBITOR 3, EXONS 1-4) - RATTUS NORVEGICUS (RAT), 1487 aa.	3.20E-127	
772	cg43960639	987	CCATGCTCTGGG AGAATGGGAGC CTC[A/C]TCGCC CACTTGAAAGTC AAAGTAGA	A	C	Asp	Glu (1145)	CONSERVATIVE	UNCLASSIFIED	Human Gene Homologous to TREMBLIN-ACC:CAB40416 P24B PROTEIN PRECURSOR - HOMO SAPIENS (HUMAN), 217 aa.	9.00E-111	
773	cg43325007	1098	GTGGATATATGT GGCCTGCAGTA TG[G/A]CCACACA GCTTCTCCTGG AGGCTGCC	G	A	Ala	Val (1146)	CONSERVATIVE	UNCLASSIFIED	Human Gene Homologous to TREMBLIN-ACC:AAD43195 PEROXISOMAL MEMBRANE PROTEIN PMP 24 - HOMO SAPIENS (HUMAN), 212 aa.	4.80E-110	20
774	cg42907145	853	GCCACCTCCCA TAACCTTCTCAG CA[G/A]CATAGA CTGACTTGCCA CATCGAGG	G	A	Ala	Val (1147)	CONSERVATIVE	UNCLASSIFIED	Human Gene Homologous to SWISSPROT-ACC:P50461 LIM DOMAIN PROTEIN, CARDIAC (MUSCLE LIM PROTEIN) (CYSTEINE-RICH PROTEIN 3) (CRP3) (LIM-ONLY PROTEIN 4) - Homo sapiens (Human), 194 aa.	1.10E-108	11
775	cg43972159	1374	AAGCCATTAGGT TCTCGGGCTGC TG[A/T]ACTGTTT GATTTTGACTTT TCCTTC	A	T	Ser	Thr (1148)	CONSERVATIVE	UNCLASSIFIED	Human Gene Homologous to SPTREMBL-ACC:Q13845 BCL7B PROTEIN - HOMO SAPIENS (HUMAN), 202 aa.	2.60E-102	7 (12q24.1)

776	cg39512856	508	CCAGGCTGTGC CGTCCACTTCT GATTAATCCC CTCCCGCGAT AACCAGGT	T	A	Tyr	Phe (1149)	CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P03740 HYPOTHETICAL PROTEIN ORF194 - Bacteriophage lambda, 194 aa.	1.20E-98	
777	cg28461713	584	TCTGCAATTGG CTCCTGGGCAT GG[G/A]CAGCTT GCAGCTGAAGT TGGTTGTA	G	A	Ala	Val (1150)	CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P47710 ALPHA-S1 CASEIN PRECURSOR - Homo sapiens (Human), 185 aa.	5.90E-96	4 (4q21.1)
778	cg43969092	361	CGGCGCCCGTC ATCACGGATGT GCA[C/A]GTCCC CGTCGGTCAGC AGCAGCACA	C	A	Val	Leu (1151)	CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:BAA74913 KIAA0890 PROTEIN - HOMO SAPIENS (HUMAN), 1194 aa.	6.30E-89	
779	cg42688841	487	GGTCATAGTAT AAAGAAGGCTT GA[C/T]GACAAA CAGTCTCTGCC ATGGTCC	C	T	Val	Ile (1152)	CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:Q02380 NADH-UBIQUINONE OXIDOREDUCTASE SGD SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-SGDH) (CI-SGDH) - Bos taurus (Bovine), 189 aa.	1.90E-83	
780	cg39523553	603	GACGCGTTGGT TCCCGACGAAG ACG[C/T]CCGAG CGGCCAAGTGG GCGGTGGCG	C	T	Ala	Val (1153)	CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:CAB40855 PUTATIVE ADENINE GLYCOSYLASE - STREPTOMYCES COELICOLOR, 308 aa.	7.20E-75	
781	cg39523553	819	ATGGACGTGGT GCGCAACAGCC CTC[A/G]CGGAG TGAAGGTCCAG ATGGCTCTT	A	G	His	Arg (1154)	CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:CAB40855 PUTATIVE ADENINE GLYCOSYLASE - STREPTOMYCES COELICOLOR, 308 aa.	7.20E-75	

782	cg39523553	857	CCAGATGGCTC TTTCCGCCTGG CCQ[G/C]JAGCTC GATCAGGCATC AAGTGCCT	G	C	Glu	Gln (1155)	CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:CAB40855 PUTATIVE ADENINE GLYCOSYLASE - STREPTOMYCES COELICOLOR, 308 aa.	7.20E-75
783	cg35933325	274	AACCACAGAGA ATACAGTGACAA CA/ATJAGAAAC AAATGACCAAA TGCCACT	A	T	Phe	Tyr (1156)	CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:BAA74845 KIAA0822 PROTEIN - HOMO SAPIENS (HUMAN), 1581 aa.	2.40E-74
784	cg41677120	544	GTTGTTTAACTT AAGCAATTTTT G[G/A]ATAAAAG TGGATTGCAAG GATATGA	G	A	Asp	Asn (1157)	CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q13492 CALM (TYPE I CALM PROTEIN) - HOMO SAPIENS (HUMAN), 652 aa.	1.10E-71
785	cg43951096	2850	AACATCAACAAT CGTTATTGGGTC TT[C/T]ATTTTTG CTAGAAGAAAGTA TCTGG	T	C	Lys	Arg (1158)	CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q23382 ZK1058.4 - CAENORHABDITIS ELEGANS, 442 aa.	2.00E-71
786	cg42696021	444	GCTGTGCCGCC TTCACAAATGAAG TG[A/G]ACCGGA AGCTGGGCAAG CCTGATTT	A	G	Asn	Asp (1159)	CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P55789 AUGMENTER OF LIVER REGENERATION (HERV1 PROTEIN) - Homo sapiens (Human), 125 aa.	1.40E-69
787	cg34243633	447	GCTGGCACCCGA CATAAGAACTTG TT[T/C]TCCAGCT GGGAGCAGCA TGGCAAC	T	C	Lys	Arg (1160)	CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O88552 CLAUDIN-2 - MUS MUSCULUS (MOUSE), 230 aa.	1.30E-68
788	cg34243633	472	TTCCAGCTGGG GAGCAGCATGG CAA[C/T]CAGTG TGCCCAAAAGC CCCAGAAAGG	C	T	Val	Ile (1161)	CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O88552 CLAUDIN-2 - MUS MUSCULUS (MOUSE), 230 aa.	1.30E-68

789	cg43942922	268	GTCCTCTGTCAA GACCCCTGAAA CA[G/A]TTGTCC CCACAGCCCT GAGCTCCA	G	A	Val	Ile (1162)	CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q14676 KIAA0170 PROTEIN - HOMO SAPIENS (HUMAN), 2089 aa.	2.30E-68	
790	cg43942922	310	TGAGCTCCAGC CTTCCACCTCCA CA[G/A]ACCAGC CTGTCACCTCTG AGCCAC	G	A	Asp	Asn (1163)	CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q14676 KIAA0170 PROTEIN - HOMO SAPIENS (HUMAN), 2089 aa.	2.30E-68	
791	cg44938009	1139	TTCTGTCAATGT GGTCCGTGCCA TG[A/G]TTGATAA CTGGGATGTCC TCTTCCA	A	G	Ile	Val (1164)	CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:Q43182 RHO-GTPASE- ACTIVATING PROTEIN 6 (RHO- TYPE GTPASE-ACTIVATING PROTEIN RHOGAPX-1) - Homo sapiens (Human), 587 aa.	5.80E-66	X
792	cg39516123	631	AGCCCTCAGGC GCGCCACAGAA CAGT[G/G]GGCA CCAACACTCCC CCTAGTCCT	T	G	Val	Gly (1165)	CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q04205 TENSIN - Gallus gallus (Chicken), 1744 aa.	5.10E-62	
793	cg44921974	279	GATTATGTCGCC GTTGAGTTCGG TC[A/G]CAGACT TGATGTTTTGA AAGTTGT	A	G	Val	Ala (1166)	CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P07148 FATTY ACID-BINDING PROTEIN, LIVER (L-FABP) - Homo sapiens (Human), 127 aa.	1.6E-61	2 (4q28)
794	cg42731307	497	AAGGCATTGAT GATCCGGTCCC CCA[G/C]TGGGT TGATGGCAAGTT CTGGAATC	G	C	Leu	Val (1167)	CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q99653 CALCIUM-BINDING PROTEIN P22 (CALCIUM-BINDING PROTEIN CHP) - Homo sapiens (Human), 194 aa.	2.60E-61	
795	cg42731307	534	CAAGTCTGGAA TCCTCTGGAAT C[T/G]TCCCGGC TGAGAGTCCCA TTCTCTC	T	G	Glu	Asp (1168)	CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q99653 CALCIUM-BINDING PROTEIN P22 (CALCIUM-BINDING PROTEIN CHP) - Homo sapiens (Human), 194 aa.	2.60E-61	

796	cg44015614	1330	TCCACAACTTCT TCTGATGAGATG TTT/CJCTCCATTT CCATGTGTTTGT CCAAG	T	C	Asn	Asp (1169)	CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P91343 HYPOTHETICAL 49.0 KD TRP-ASP REPEATS CONTAINING PROTEIN F55F8.5 IN CHROMOSOME I - Caenorhabditis elegans, 439 aa.	3.30E-54	
797	cg43298242	143	GATCTGTTGGC AGGGCTCACAG AGA[C/T]GGGG TGAGGGGAGAG ATCGTGGGT	C	T	Val	Ile (1170)	CONSERVATI VE	water_ch annel	Human Gene SWISSPROT- ID:O14520 AQUAPORIN-7 LIKE (AQUAPORIN ADIPOSE) (AQPAP) - HOMO SAPIENS (HUMAN), 342 aa.	1.3E-163	
798	cg43299610	842	CTCCAGTGCC CGCCCGACTAC CAC[C/T]ACATC CACACCGAGAT CTCCCGGGA	C	T	His	Tyr (1171)	NON- CONSERVATI VE	ATPase_ associat ed	Human Gene Homologous to SWISSPROT-ID:P39986 PROBABLE CALCIUM-TRANSPORTING ATPASE 6 (EC 3.6.1.38) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 1215 aa.	1.40E-109	
799	cg42532480	564	TTTCCTGAATGA ATGTTAAAGATT CTT/AJGTCAAG TCAGTATGCG ATCCAAG	T	A	Arg	End (1172)	NON- CONSERVATI VE	cadherin	Human Gene Homologous to SWISSPROT-ID:P79995 CADHERIN- 10 PRECURSOR - GALLUS GALLUS (CHICKEN), 789 aa. pcis:SPTREMBL- ID:P79995 CADHERIN-10 - GALLUS GALLUS (CHICKEN), 789 aa.	6.00E-115	
800	cg42926989	259	GCAATGAGCTG CTGGCAGCACA AAG[G/T]CTTATC GCACCAGGAAA GATGCAGC	G	T	Ala	Asp (1173)	NON- CONSERVATI VE	cathepsi n	Human Gene Homologous to SWISSPROT-ID:P08311 CATHESPIN G PRECURSOR (EC 3.4.21.20) - HOMO SAPIENS (HUMAN), 255 aa.	1.7E-136 (14q11.2)	14
801	cg43991318	2521	TGGTCCGGGAA TACCTGGTGA CCCTT/GJCGGG CCCGCTGCCA GGAGCTGCC	T	G	Cys	Gly (1174)	NON- CONSERVATI VE	collagen	Human Gene Similar to SWISSPROT- ID:Q07092 COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1603 aa.	1.3E-73 1 (1p34)	

807	cg43312829	1402	TAGTGAAAATCT CCAATCAAAGAC A A G C A G G A C T CCATGTAAGTGA ATATGA	A	G	Thr	Ala (1180)	NON- CONSERVATIVE	dehydrogenase	Human Gene SWISSPROT- ID:Q16134 ELECTRON TRANSFER FLAVOPROTEIN-UBIQUINONE OXIDOREDUCTASE PRECURSOR (EC 1.5.5.1) (ETF-QO) (ETF- UBIQUINONE OXIDOREDUCTASE) (ETF DEHYDROGENASE) (ELECTRON-TRANSFERRING- FLAVOPROTEIN DEHYDROGENASE) - HOMO SAPIENS (HUMAN), 617 aa.	0	4
808	cg43959136	1144	TGGGCCAACAA GCTTGAGTGCG ATC C T GGTCT GCAATGATGGA GGAATTGCC	C	T	Arg	Gln (1181)	NON- CONSERVATIVE	dehydrogenase	Human Gene SWISSPROT-ID:P11586 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC (C1- THF SYNTHASE) (METHYLENETETRAHYDROFOLAT E DEHYDROGENASE (EC 1.5.1.5) / METHENYLTETRAHYDROFOLATE CYCLOHYDROLASE (EC 3.5.4.9) / FORMYLTETRAHYDROFOLATE SYNTHETASE (EC 6.3.4.3)) - HOMO SAPIENS (HUMAN), 934 aa. pcls:SWISSPROT-ID:P11586 C-1- TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC (METHYLENETETRAHYDROFOLAT E DEHYDROGENASE (EC 1.5.1.5) / METHENYLTETRAHYDROFOLATE CYCLOHYDROLASE (EC 3.5.4.9) / FORMYLTETRAHYDROFOLATE SYNTHETASE (EC 6.3.4.3)) (C1-THF SYNTHASE) - HOMO SAPIENS (HUMAN), 934 aa.	0	14

809	cg43969759	648	TGTCAGGAGGA AGATCTCATCTG GG[A/G]TGTGCC GGATCCCGCG GCGATGAC	A	G	Ile	Thr (1182)	NON- CONSERVATI VE	dehydrog enase	Human Gene Homologous to SPTREMBL-ID:Q16797 NADP- DEPENDENT MALIC ENZYME (EC 1.1.1.40) (MALATE DEHYDROGENASE (OXALOACETATE DECARBOXYLATING) (NADP+)) (PYRUVIC-MALIC CARBOXYLASE) - HOMO SAPIENS (HUMAN), 572 aa. Human Gene Similar to SWISSPROT- ID:P46703 ACYL-COA DEHYDROGENASE (EC 1.3.99.-) - MYCOBACTERIUM LEPRAE, 389 aa.	1.8E-109	11
810	cg39523614	697	GGGAGCTTTAG ACATTGCCACG GATT[C/J]ACGTC CAGAAAGCGCAA GCAGTTTGG	T	C	Tyr	His (1183)	NON- CONSERVATI VE	dehydrog enase		2.10E-76	
811	cg42175288	1152	TGGAGACCCCA AAAGTGGGGAT TGG[G/T]TTTGC CCTAATCCGTCA TGCGGAAA	G	T	Val	Phe (1184)	NON- CONSERVATI VE	dna_rna _bind	Human Gene SPTREMBL-ID:Q92804 PUTATIVE RNA BINDING PROTEIN RBP56 - HOMO SAPIENS (HUMAN), 592 aa.	0.00E+00	17
812	cg43154217	1352	GCAGAAAGAGGT GATTGTGAGAG GAC[C/A]AAGAG CTCCAGGAACA GCTGGAACT	C	A	Gly	Cys (1185)	NON- CONSERVATI VE	dna_rna _bind	Human Gene Similar to SWISSPROT- ID:P26599 POLYPYRIMIDINE TRACT-BINDING PROTEIN (PTB) (HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN I) (HNRNP I) (57 KD RNA-BINDING PROTEIN PPTB-1) - HOMO SAPIENS (HUMAN), 531 aa.	2.20E-90	
813	cg39709402	108	GGAACACATTAA TAAACAAGTAGA A[G/C]CCTACAG AGAGGAATCGC AAAAATC	G	C	Ala	Pro (1186)	NON- CONSERVATI VE	dna_rna _bind	Human Gene Similar to SPTREMBL- ID:O08872 PUTATIVE RNA BINDING PROTEIN 1 - RATTUS NORVEGICUS (RAT), 362 aa (fragment).	3.20E-57	
814	cg39709402	133	GCCTACAGAGA GGAATCGCAA AAT[C/G]CCTGA AAGAATTCCAG GAAAAACACA	C	G	Ser	Cys (1187)	NON- CONSERVATI VE	dna_rna _bind	Human Gene Similar to SPTREMBL- ID:O08872 PUTATIVE RNA BINDING PROTEIN 1 - RATTUS NORVEGICUS (RAT), 362 aa (fragment).	3.20E-57	

815	cg39709402	57	GATGCTGGAGG ACTTCAAGAAAG AC(A/G)TGAAGA ACTCCCTTAGAG AAACACA	A	G	Met (1188)	Val (1188)	NON- CONSERVATI VE	dna_rna _bind	Human Gene Similar to SPTREMBL- ID:O08872 PUTATIVE RNA BINDING PROTEIN 1 - RATTUS NORVEGICUS (RAT), 362 aa (fragment).	3.20E-57	
816	cg39709402	76	AAAGACATGAA GAACTCCCTTAG AG(A/G)AACACA GAAACACATTAA TAAACAA	A	G	Glu (1189)	Gly (1189)	NON- CONSERVATI VE	dna_rna _bind	Human Gene Similar to SPTREMBL- ID:O08872 PUTATIVE RNA BINDING PROTEIN 1 - RATTUS NORVEGICUS (RAT), 362 aa (fragment).	3.20E-57	
817	cg39709402	94	CTTAGAGAAACA CAGGAAAACATT A(A/G)TAAACAA GTAGAAGCCTA CAGAGAG	A	G	Asn (1190)	Ser (1190)	NON- CONSERVATI VE	dna_rna _bind	Human Gene Similar to SPTREMBL- ID:O08872 PUTATIVE RNA BINDING PROTEIN 1 - RATTUS NORVEGICUS (RAT), 362 aa (fragment).	3.20E-57	
818	cg39709402	96	TAGAGAAACACA GGAAACATTAA T(A/G)AACAAAGT AGAAGCCTACA GAGAGGA	A	G	Lys (1191)	Glu (1191)	NON- CONSERVATI VE	dna_rna _bind	Human Gene Similar to SPTREMBL- ID:O08872 PUTATIVE RNA BINDING PROTEIN 1 - RATTUS NORVEGICUS (RAT), 362 aa (fragment).	3.20E-57	
819	cg43950268	1949	TTTGCTATGTCC TCCTTGACCTCC T(G/A)CTCGGTG GCGGTCACAAT GCCCTCC	G	A	Gln (1192)	End (1192)	NON- CONSERVATI VE	eph	Human Gene TREMBLNEW- ID:G2865466 HEAT SHOCK PROTEIN 75 - HOMO SAPIENS (HUMAN), 649 aa.	0.00E+00	16
820	cg43985169	540	AAGACGAATGG GTGGTGGTAGA GAT(T/C)CTGAA GAAATGGAAATA GATGGTGA	T	C	Ser (1193)	Pro (1193)	NON- CONSERVATI VE	eph	Human Gene Homologous to SWISSPROT-ID:P25685 DNAJ PROTEIN HOMOLOG 1 (HDJ-1) (HEAT SHOCK PROTEIN 40) (HSP40) - HOMO SAPIENS (HUMAN), 340 aa.	2.40E-123	
821	cg43997616	2250	AAAGCCAGCGG AGCCGTAAGCA TCA(T/C)ACTGCT TCCTCTTCACCT CATCACT	T	C	Tyr (1194)	Cys (1194)	NON- CONSERVATI VE	eph	Human Gene Similar to TREMBLNEW-ID:G2735762 HEAT SHOCK PROTEIN DNAJ - LEPTOSPIRA INTERROGANS, 369 aa.	1.40E-55	

822	cg43319420	992	CACGACAACCTA CAGAAACAACCC CCTT/C]CCACA ACTTCGGGCAC TGCTTCTGC	T	C	Phe	Ser (1195)	NON- CONSERVATIVE	esterase	Human Gene Similar to SWISSNEW- ID:Q23917 3'-5'-CYCLIC- NUCLEOTIDE PHOSPHODIESTERASE REGA (EC 3.1.4.17) (PDEASE REGA) - DICTYOSTELIUM DISCOIDEUM (SLIME MOLD), 793 aa.lpcis:SWISSPROT-ID:Q23917 3'-5'- CYCLIC-NUCLEOTIDE PHOSPHODIESTERASE REGA (EC 3.1.4.17) (PDEASE REGA) - DICTYOSTELIUM DISCOIDEUM (SLIME MOLD), 793 aa.	3.30E-60	21
823	cg44034764	382	GAGGTCCAGGC TGGGCAGGACA GTC/T/C]CCCCA TGGTGCCGTA CAGCCTCTT	T	C	Glu	Gly (1196)	NON- CONSERVATIVE	glycoprotein	Human Gene SWISSPROT- ID:P23276 KELL BLOOD GROUP GLYCOPROTEIN (EC 3.4.24.-) - HOMO SAPIENS (HUMAN), 732 aa.	0.00E+00	7 (Xp21.2)
824	cg43991224	217	TCTCATCTGTCT ACCTACAGCCT GGT/A]TTGGGT CATGGCAGCAG TGGTGCTG	T	A	Val	Asp (1197)	NON- CONSERVATIVE	glycoprotein	Human Gene Homologous to SWISSPROT-ID:P41217 OX-2 MEMBRANE GLYCOPROTEIN PRECURSOR - HOMO SAPIENS (HUMAN), 274 aa (fragment).	1.50E-139	
825	cg44018623	1824	TACCATCTCTGT TTTTACCACTGG T[G/A]GCTCTGA ACAACAAATAAT TTGTGG	G	A	Pro	Leu (1198)	NON- CONSERVATIVE	glycoprotein	Human Gene Homologous to SPTREMBL-ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa.	1.90E-114	6
826	cg38924741	598	AAAGAGGAGAA TGGTGACTTTTGC CTT/C]ATTTCAGA GTGGAACGAGC TGAAAGG	T	C	Leu	Ser (1199)	NON- CONSERVATIVE	glycoprotein	Human Gene Similar to SWISSPROT- ID:P04196 HISTIDINE-RICH GLYCOPROTEIN PRECURSOR (HISTIDINE-PROLINE RICH GLYCOPROTEIN) (HPRG) - HOMO SAPIENS (HUMAN), 525 aa.	3.30E-55	

827	cg43322513	13082	TTCCTGTTCTTC ACATGGTGAGC CC[C]/TGGCCCTG CTGTCTGCTTGC ATTGGGG	C	T	Arg	Gln (1200)	NON- CONSERVATIVE	glycoprotein	Human Gene Similar to SWISSPROT- ID:P13983 EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE- RICH GLYCOPROTEIN) - NICOTIANA TABACUM (COMMON TOBACCO), 620 aa.	3.30E-54	12
828	cg44913214	2306	GAACACAACAAA GAAAAAACAGA GT[C]/TTGGGAC TCATCCAAAAGG GACGAGA	C	T	Ser	Phe (1201)	NON- CONSERVATIVE	helicase	Human Gene TREMBLNEW- ID:G2801555 PUTATIVE ATP- DEPENDENT MITOCHONDRIAL RNA HELICASE - HOMO SAPIENS (HUMAN), 786 aa.	0.00E+00	10
829	cg39529972	278	TTGGCCTCGAC ATCATCCCTGA CG[A]/GGACTT AAAGGGTAGCA ATTCGIAT	A	G	Ser	Pro (1202)	NON- CONSERVATIVE	hydrolase	Human Gene Similar to SWISSPROT- ID:Q01477 UBIQUITIN CARBOXYL- TERMINAL HYDROLASE 3 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 3) (UBIQUITIN- SPECIFIC PROCESSING PROTEASE 3) (DEUBIQUITINATING ENZYME 3) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 912 aa.	1.00E-52	
830	cg43925670	2309	TAGTTTGCCCAA ACCAGCATCAC CT[C]/G]GGAAC TTTCTTCCATCA AGTCAGC	C	G	Arg	Pro (1203)	NON- CONSERVATIVE	interferon	Human Gene SWISSPROT- ID:Q16666 GAMMA-INTERFERON- INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa.pcls:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment)	0.00E+00	1

831	cg43925670	2369	TTTGTCATCTC TTCTCTCATTTT T(A/G)AATTAAAGT TTTAAATCGTTG CTCAG	A	G	Leu	Ser (1204)	NON- CONSERVATIVE	interferon	Human Gene SWISSPROT- ID:Q16666 GAMMA-INTERFERON- INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa.lpcsls:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment)	0.00E+00	1
832	cg43925670	2458	CCTCTAATCCTT TTAGTAGAACAA T(G/T)TCTTGTA TTTTTTTCCCAT CTTTA	G	T	Asn	Lys (1205)	NON- CONSERVATIVE	interferon	Human Gene SWISSPROT- ID:Q16666 GAMMA-INTERFERON- INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa.lpcsls:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment)	0.00E+00	1
833	cg43925670	2467	CTTTTAGTAGAA CAATGTTCTTGT A(T/G)TTTTTCC CATCTTTACAGA CATAA	T	G	Lys	Asn (1206)	NON- CONSERVATIVE	interferon	Human Gene SWISSPROT- ID:Q16666 GAMMA-INTERFERON- INDUCIBLE PROTEIN IFI-16 (INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa.lpcsls:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment)	0.00E+00	1

834	cg43331742	845	TCCTCGAGGTG CTTCCACACAGA CTC[G/A]ATTTCT GAGTTTCCACA GAAAAGA	G	A	Ser	Leu (1207)	NON- CONSERVATIVE	isomerase	Human Gene Homologous to SWISSPROT-ID:P70473 2- ARYLPROPIONYL-COA EPIMERASE (EC 5.-.-) - RATTUS NORVEGICUS (RAT), 361 aa.	5.60E-131	
835	cg43253796	1812	GAAATGGATCTT ATTGGACTTTG C[G/T]ACAAAGAC TGCCGAGAGAT TTTCCCA	G	T	Arg	Leu (1208)	NON- CONSERVATIVE	kinase	Human Gene SWISSNEW-ID:P42338 PHOSPHATIDYLINOSITOL 3- KINASE CATALYTIC SUBUNIT, BETA ISOFORM (EC 2.7.1.137) (PI3- KINASE P110 SUBUNIT BETA) (PTDINS-3-KINASE P110) (PI3K) - HOMO SAPIENS (HUMAN), 1070 aa.lpcis:SWISSPROT-ID:P42338 PHOSPHATIDYLINOSITOL 3- KINASE CATALYTIC SUBUNIT, BETA ISOFORM (EC 2.7.1.137) (PI3- KINASE P110 SUBUNIT BETA) (PTDINS-3-KINASE P110) (PI3K) - HOMO SAPIENS (HUMAN), 1070 aa	0.00E+00	
836	cg43257400	2094	GACATCAGCAT GGCTGCCCCCG ACTT[C/C]CAGCA GAACATGATCAT TCTCTGAC	T	C	Ser	Pro (1209)	NON- CONSERVATIVE	kinase	Human Gene SPTREMBL-ID:Q60680 CONSERVED HELIX-LOOP-HELIX UBIQUITOUS KINASE - MUS MUSCULUS (MOUSE), 745 aa.	0.00E+00	10
837	cg43974480	686	TCACGGACTTTG GACTGTCCAAAA T[G/T]GGCCTCA TGAGCCTGACA ACGAAC	G	T	Met	Ile (1210)	NON- CONSERVATIVE	kinase	Human Gene SPTREMBL-ID:O00114 HYPOTHETICAL HUMAN SERINE- THREONINE PROTEIN KINASE R31240_1 - HOMO SAPIENS (HUMAN), 1237 aa (fragment).	0.00E+00	
838	cg43922705	4337	CAAACCGGCTTT CTCCATGGTGC CC[T/C]GCCAAA CCCTGGAGTTC CCAGGCTG	T	C	Gln	Arg (1211)	NON- CONSERVATIVE	kinase	Human Gene SWISSPROT- ID:P27987 1D-MYO-INOSITOL- TRISPHOSPHATE 3-KINASE B (EC 2.7.1.127) (INOSITOL 1,4,5- TRISPHOSPHATE 3-KINASE) (IP3K) (IP3 3-KINASE) - HOMO SAPIENS (HUMAN), 505 aa (fragment).	3.80E-279	1 (1q41)

851	cg44019843	929	GAGTGACCCGC CTCCCTGGTCC AAGATATATGTG GAGTACACCTTC ACAGGGAT	A	T	Asn	Tyr (1224)	NON- CONSERVATI VE	misc_ch annel	Human Gene SPTREMBL-ID:Q15478 SODIUM CHANNEL ALPHA SUBUNIT - HOMO SAPIENS (HUMAN), 1836 aa.	0.00E+00	17 (17q23.1)
852	cg44128805	1396	AGTGCACACAG TGAGCTCAGAG CTT[C/T]CCCCCT GAAACCCGAAA GTTTCAACT	C	T	Glu	Lys (1225)	NON- CONSERVATI VE	nuclease	Human Gene Similar to SWISSPROT- ID:P54278 PMS1 PROTEIN HOMOLOG 2 (DNA MISMATCH REPAIR PROTEIN PMS2) - HOMO SAPIENS (HUMAN), 862 aa.	1.60E-76	7
853	cg38642684	304	TTTCTGATAATC ATTTAAGGTATG T[A/T]AGTTGCTA GTATTTAATTTA ACCTT	A	T	Leu	End (1226)	NON- CONSERVATI VE	nuclease	Human Gene Similar to SWISSNEW- ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] - HOMO SAPIENS (HUMAN), 874 aa.lpcIs:SWISSPROT-ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) - HOMO SAPIENS (HUMAN), 874 aa.	2.60E-50	
854	cg38642684	417	CTTTTCAGGTG CAATGATTAAAC C[A/T]CTTAACTG TGCATTCTTAT GACAG	A	T	Ser	Arg (1227)	NON- CONSERVATI VE	nuclease	Human Gene Similar to SWISSNEW- ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] - HOMO SAPIENS (HUMAN), 874 aa.lpcIs:SWISSPROT-ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) - HOMO SAPIENS (HUMAN), 874 aa.	2.60E-50	

855	cg44913844	1194	CCAGTTGGTAAA CTGGTCTTAAAC C[G/A]GAATCCA GTTAATTACTTT GCTGAG	G	A	Arg	Gln (1228)	NON- CONSERVATI VE	peroxidase	Human Gene SWISSPROT- ID:P04040 CATALASE (EC 1.11.1.6) - HOMO SAPIENS (HUMAN), 527 aa.	2.70E-296	11 (11p13)
856	cg40084915	5005	CCTGCGGTCTG GGGAGATGAGG GCC[T/C]CAAAC AGCACCTGATAT TCATTGGG	T	C	Glu	Gly (1229)	NON- CONSERVATI VE	phosphatase	Human Gene SPTREMBL-ID:O00197 RECEPTOR PROTEIN TYROSINE PHOSPHATASE HPTP-J PRECURSOR - HOMO SAPIENS (HUMAN), 1436 aa.	0.00E+00	1
857	cg42720088	214	AAAGCTCAGAG AGATCTGGGCT ATG[A/T]GCCAC TTGTCAGCTGG GAGGAAGCC	A	T	Glu	Val (1230)	NON- CONSERVATI VE	reductase	Human Gene Similar to SWISSPROT- ID:P22072 3 BETA- HYDROXYSTEROID DEHYDROGENASE/DELTA 5->4- ISOMERASE TYPE II (3BETA-HSD II) (3-BETA-HYDROXY-DELTA(5)- STEROID DEHYDROGENASE (EC 1.1.1.145) (3-BETA-HYDROXY-5- ENE STEROID DEHYDROGENASE) (PROGESTERONE REDUCTASE) / STEROID DELTA-ISOMERASE (EC 5.3.3.1) (DELTA-5-3-KETOSTEROID ISOMERASE)) - RATTUS NORVEGICUS (RAT), 372 aa.	2.40E-50	
858	cg43957486	1528	CGCTCCTGCAC CGCATCCGCGA CGC[A/T]GTCCT GCAACGACCTC TGCAGGCAC	A	T	Gln	Leu (1231)	NON- CONSERVATI VE	struct	Human Gene SWISSPROT- ID:P07204 THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM) (CD141 ANTIGEN) - HOMO SAPIENS (HUMAN), 575 aa.	0.00E+00	20 (20p11.2)
859	cg40148056	1462	CTCAGAGACCC CTAACAACCCA GCA[G/C]CCACA GAGCGGAACAC TTAAGGATC	G	C	Gln	His (1232)	NON- CONSERVATI VE	struct	Human Gene SPTREMBL-ID:Q92777 SYNAPSIN IIB - HOMO SAPIENS (HUMAN), 478 aa.	2.90E-260	3 (3p)

863	cg43297806	994	TGCAGGGAGCG TAGTGCCAGAG GGG[T/C]CTGGG AGGAGGCTGAA ATCACCTGA	T	C	Thr	Ala (1236)	NON- CONSERVATI VE	sulfotran sferase	Human Gene SWISSPROT- ID:P52849 HEPARIN SULFATE N- DEACETYLASE/N- SULFOTRANSFERASE (EC 2.8.2.-) (N- HSST) (N-HEPARIN SULFATE SULFOTRANSFERASE) (GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE) - HOMO SAPIENS (HUMAN), 883 aa.pclis:TREMBLNEW-ID:G2792518 HEPARAN GLUCOSAMINYL N- DEACETYLASE/N- SULFOTRANSFERASE-2 - HOMO SAPIENS (HUMAN), 883 aa	0.00E+00	10
864	cg43987111	1337	AGTAGTCTGCG TCTCCATAGAGT TT[C/A]CTCATGA CTGAGTCTTGG TCTGGA	C	A	Arg	Ser (1237)	NON- CONSERVATI VE	synthase	Human Gene SWISSPROT- ID:P17812 CTP SYNTHASE (EC 6.3.4.2) (UTP--AMMONIA LIGASE) (CTP SYNTHETASE) - HOMO SAPIENS (HUMAN), 591 aa	0.00E+00	18 (1p34.1)
865	cg43976335	633	GAAATGCACGTG GACCACTCGGG CAG[G/A]GCTGC CAGGCCGTAGC AGGCAATTC	G	A	Pro	Ser (1238)	NON- CONSERVATI VE	synthase	Human Gene SWISSPROT- ID:P48637 GLUTATHIONE SYNTHETASE (EC 6.3.2.3) (GLUTATHIONE SYNTHASE) (GSH SYNTHETASE) (GSH-S) - HOMO SAPIENS (HUMAN), 474 aa	5.30E-240 (20q11.2)	20
866	cg39515668	605	ACGCACGAACC GGTCATACTGG TCG[G/T]TGATC CAGGAACGGTC GCACAGCTG	G	T	Thr	Asn (1239)	NON- CONSERVATI VE	synthase	Human Gene Similar to SWISSNEW- ID:P54876 PHOSPHORIBOSYLFORMYLGLYCI NAMIDINE SYNTHASE II (EC 6.3.5.3) (FGAM SYNTHASE II) - MYCOBACTERIUM TUBERCULOSIS, 754 aa	2.80E-72	
867	cg44027791	1261	GAAGCGCTTCT GACACTGGGCG CAC[T/C]CGAAG CGTTTGTCCTCCT GTGIGGGT	T	C	Glu	Gly (1240)	NON- CONSERVATI VE	transcript factor	Human Gene SWISSPROT- ID:Q02086 TRANSCRIPTION FACTOR SP2 (KIAA0048) - HOMO SAPIENS (HUMAN), 606 aa	0.00E+00	17

868	cg43992817	578	GAGGGGCCGCT GGAAGGTGACA CTG[C]/TGTGG GGCCACGGAG GTGCCGCTG	C	T	Ala	Thr (1241)	NON- CONSERVATIVE	transcript factor	Human Gene Homologous to SWISSNEW-ID:Q14469 TRANSCRIPTION FACTOR HES-1 (HAIRY AND ENHANCER OF SPLIT 1) (HAIRY- LIKE) (HHL) (HAIRY HOMOLOG) - HOMO SAPIENS (HUMAN), 280 aa.	1.50E-144	3
869	cg43297259	816	TAAGTGTCTGAT GAGGTGTGACT TC[T]/CGGCTAA AGCCTTGCTCA CACTCCCT	T	C	Gln	Arg (1242)	NON- CONSERVATIVE	transcript factor	Human Gene Similar to SWISSNEW- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa. pcis:SWISSPROT- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.	7.80E-54	
870	cg42716761	1594	CGAGAAGACCC TATACCATCACG TG[C]/GJACGGCT GCGACGTGTTT CACCTCCG	C	G	His	Asp (1243)	NON- CONSERVATIVE	transcript factor	Human Gene SWISSNEW-ID:Q61079 SINGLE-MINDED HOMOLOG 2 (SIM TRANSCRIPTION FACTOR) (MSIM) - MUS MUSCULUS (MOUSE), 657 aa. pcis:SWISSPROT-ID:Q61079 SINGLE-MINDED HOMOLOG 2 (SIM TRANSCRIPTION FACTOR) (MSIM) - MUS MUSCULUS (MOUSE), 657 aa.	5.7e-312	21
871	cg42166807	2828	AGAGCAATGGC TCTCTTCACTCC GT[G]/A/GAAGTT GTCCTCTCAGAA GCTGGGC	G	A	Trp	End (1244)	NON- CONSERVATIVE	transferrase	Human Gene SWISSPROT- ID:Q09328 ALPHA-1,3(6)- MANNOSYLGLYCOPROTEIN BETA- 1,6-N-ACETYL- GLUCOSAMINYLTRANSFERASE V (EC 2.4.1.155) (ALPHA-MANNOSIDE BETA-1,6-N- ACETYLGLUCOSAMINYLTRANSFERASE) (N-ACETYLGLUCOSAMINYL- TRANSFERASE V) (GNT-V) (GLCNAC-T V) - HOMO SAPIENS (HUMAN), 741 aa.	0.00E+00	2 (2q21)

872	cg38869466	752	TTCACCTTGATT AACGTCCTGGT CC[T/C]GGGCTT CATAATGGTGTC AGGATT	T	C	Leu	Pro (1245)	NON- CONSERVATIVE	transport	Human Gene SWISSPROT- ID:P30825 HIGH-AFFINITY CATIONIC AMINO ACID TRANSPORTER-1 (CAT-1) (CAT1) (SYSTEM Y+ BASIC AMINO ACID TRANSPORTER) (ECOTROPIC RETROVIRAL LEUKEMIA RECEPTOR HOMOLOG) (ERR) (ECOTROPIC RETROVIRUS RECEPTOR HOMOLOG) - HOMO SAPIENS (HUMAN), 629 aa.	0.00E+00	13
873	cg42742340	3392	CAGAGAGACGG TGTCATCAGCA TC[C/T]GGGCT CCCTGCAGCAG ACCCAGGC	C	T	Arg	Trp (1246)	NON- CONSERVATIVE	transport	Human Gene SWISSPROT- ID:Q04671 P PROTEIN (MELANOCYTE-SPECIFIC TRANSPORTER PROTEIN) - HOMO SAPIENS (HUMAN), 838 aa.	0.00E+00	1
874	cg43976701	513	TGGTATATCTGA ACTGAATCAGC CT[G/C]CTGAAC TTTTACCTCAGT TTTCTAG	G	C	Ala	Pro (1247)	NON- CONSERVATIVE	transport	Human Gene SWISSPROT- ID:Q15436 PROTEIN TRANSPORT PROTEIN SEC23 HOMOLOG ISOFORM A - HOMO SAPIENS (HUMAN), 765 aa.	0.00E+00	
875	cg43920728	2024	GTAAGTCTCATT GTAAATTTGTTG C[A/G]TGAGCAG TGCTGGGGAGT TGACAGC	A	G	Cys	Arg (1248)	NON- CONSERVATIVE	transport	Human Gene SWISSPROT- ID:P22732 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE (FRUCTOSE TRANSPORTER) - HOMO SAPIENS (HUMAN), 501 aa.	2.90E-237	1 (1p31)
876	cg43920728	2185	TGCTTGCTCTG GAAGGCAGAG TGC[C/T]GCTCA CCTCCTTTAGC CAAAGTAA	C	T	Arg	Gln (1249)	NON- CONSERVATIVE	transport	Human Gene SWISSPROT- ID:P22732 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE (FRUCTOSE TRANSPORTER) - HOMO SAPIENS (HUMAN), 501 aa.	2.90E-237	1 (1p31)

877	cg42339179	450	TCCTCCACCAG GGTCATTTTGCG GT[G/A]TTTAAAA GTTCCAGTGATC TCAATG	G	A	His	Tyr (1250)	NON- CONSERVATI VE	transport	Human Gene Homologous to SWISSNEW-ID:Q60714 LONG- CHAIN FATTY ACID TRANSPORT PROTEIN (FATP) - MUS MUSCULUS (MOUSE), 646 aa. pcls:SWISSPROT- ID:Q60714 LONG-CHAIN FATTY ACID TRANSPORT PROTEIN (FATP) - MUS MUSCULUS (MOUSE), 646 aa.	1.90E+05	15
878	cg17663981	383	TGCACCTGCGA CCAAAAACCCCT GCA[G/A]CTGCC CCAAAGGGGAT GTCAACTAC	G	A	Ser	Asn (1251)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:Q05329 GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65) (65 KD GLUTAMIC ACID DECARBOXYLASE) - Homo sapiens (Human), 585 aa.	0.00E+00	10 (10p11.2) 3
879	cg43918356	1806	GCTCCCGTGCA CGGGGCTGTAG CGC[C/T]CAGGA CTGCCCAGGCC TGGCTTTGC	C	T	Gly	Glu (1252)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O75176 KIAA0692 PROTEIN - HOMO SAPIENS (HUMAN), 783 aa (fragment).	0.00E+00	12
880	cg43924089	1080	ACCTCCTGGAG CAGTCCTGGTG TTA[C/T]ATTCCC TGCCCTCGGAG TTCCCACT	C	T	His	Tyr (1253)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA31589 KIAA0614 PROTEIN - HOMO SAPIENS (HUMAN), 1630 aa (fragment).	0.00E+00	12
881	cg43930961	2459	TTCTCCGTAGT CACAGACGTGA GG[C/T]TACTGC TTTCGGCTTCAA TGGAAAC	C	T	Ser	Asn (1254)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA20772 KIAA0313 PROTEIN - HOMO SAPIENS (HUMAN), 1499 aa.	0.00E+00	4
882	cg43966528	680	AACAACACATTC AGTACAGTGCA GC[A/G]TATCAG CAGGCCAAGTT AACCAATC	A	G	Met	Thr (1255)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O00237 HKF-1 - HOMO SAPIENS (HUMAN), 685 aa.	0.00E+00	

883	cg43980727	1367	TCCTTCCTTGTA GTCAGAGACAT CA[G/A]GAGAGT AACTGGATGTTA GCTCCAA	G	A	Pro	Leu (1256)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:P38432 P80-COILIN - Homo sapiens (Human), 576 aa.	0.00E+00	17
884	cg43981483	1540	TGACTGCATTAT TCGCAGCTGCT TA[A/G]GGACAA ATTCTACCTTCT TCITGGGT	A	G	Leu	Pro (1257)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O75882 ATTRACTIN - HOMO SAPIENS (HUMAN), 1198 aa.	0.00E+00	20
885	cg44932392	1200	TAGATGAAGGA GCCTGAGTAAG AGG[C/T]CACGC ACCAGCCTGTA GAACATATA	C	T	Trp	End (1258)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD23581 CULLIN 2 - HOMO SAPIENS (HUMAN), 745 aa.	0.00E+00	
886	cg44932924	2754	AACAGTGAGTC GGTCCAGCAGC AGA[T/C]GGAGT TCTTGAACAGG CAGCTGTIG	T	C	Met	Thr (1259)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q92574 HAMARTIN (MYELOBLAST KIAA0243) - HOMO SAPIENS (HUMAN), 1164 aa.	0.00E+00	9
887	cg43985955	2082	ACCTCCAAACC CCTTTGGCCCT GTAT[C/G]CAGGA GCACAGATACA GTTTATGTA	T	C	Ser	Pro (1260)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q13492 CALM (TYPE I CALM PROTEIN) - HOMO SAPIENS (HUMAN), 652 aa.	2.70E-299	
888	cg44002507	1373	GTCGCACCTGG CAGCCAGCAGG ATC[C/T]CGGCT ATGTCCACGCA GCCGGAGAA	C	T	Gly	Glu (1261)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD21812 G9A - HOMO SAPIENS (HUMAN), 1001 aa.	8.10E-298	
889	cg44002507	2870	TTTCCTTTCCTC TTGAGAAATTC TTT[C/G]CTTAATGC TGGATTCCGAA CTCAGG	T	C	Lys	Glu (1262)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD21812 G9A - HOMO SAPIENS (HUMAN), 1001 aa.	8.10E-298	

897	cg43258841	485	AACTCCATCCAC AAGTCCCTTGCTG A[A/G]TAATCAAT CGCTGAGCCTC ATCTCT	A	G	Ile	Thr (1270)	NON- CONSERVATIVE	UNCLASSIFIED	Human Gene SWISSNEW- ACC:Q14449 GROWTH FACTOR RECEPTOR-BOUND PROTEIN 14 (GRB14 ADAPTER PROTEIN) - Homo sapiens (Human), 540 aa.	2.70E-258	
898	cg43979679	619	GAGAAAGGAGCC CGGGAAAGTGT GAC[C/T]AGGAG AAACCGGCACC CAGCTTTGTC	C	T	Gln	End (1271)	NON- CONSERVATIVE	UNCLASSIFIED	Human Gene SPTREMBL- ACC:Q13977 MAJOR YO PARANEOPLASTIC ANTIGEN - HOMO SAPIENS (HUMAN), 509 aa (fragment).	5.60E-258	16 (16p13.1)
899	cg42202923	887	TACCCCAATGGT CTTCAGCCTCTG C[A/G]GCAGCTC CGATGAGGTCA GCTGCCG	A	G	Leu	Pro (1272)	NON- CONSERVATIVE	UNCLASSIFIED	Human Gene SPTREMBL- ACC:O75926 PROTEIN INHIBITOR OF ACTIVATED STAT PROTEIN PIASY - HOMO SAPIENS (HUMAN), 510 aa.	2.40E-256	
900	cg43320405	994	CCAGGCCTCGA ATGGACAGCAC CTT[C/A]ATGATG GGGTCGTGGTG GCTCAGGC	C	A	Met	Ile (1273)	NON- CONSERVATIVE	UNCLASSIFIED	Human Gene TREMBLNEW- ACC:CAB48424 DKFZP434G153 PROTEIN - HOMO SAPIENS (HUMAN), 466 aa.	8.20E-245	
901	cg43917689	3689	TGACAAACGCAG GCTCCAGGGGT TGT[G/A]GCTGA TCTTCTCAGAAC TCAAGCCA	G	A	His	Tyr (1274)	NON- CONSERVATIVE	UNCLASSIFIED	Human Gene SPTREMBL- ACC:Q92551 MYELOBLAST KIAA0263 - HOMO SAPIENS (HUMAN), 441 aa.	3.50E-240	3
902	cg43922856	1546	GAGAAATTCAGT GATTGGCAGAA TAG[G/A]AGATG CATGCTTGAAT TTCCAGTC	G	A	Pro	Ser (1275)	NON- CONSERVATIVE	UNCLASSIFIED	Human Gene SWISSPROT- ACC:P42167 THYMOPOIETINS BETA AND GAMMA (TP BETA AND TP GAMMA) - Homo sapiens (Human), 453 aa.	2.00E-237	12 (12q22)
903	cg43922856	1608	AACTAAGGATTC GTTGCTTGAAG CC[A/T]TTATAGT TTCAGCTATGG GAGTACT	A	T	Met	Lys (1276)	NON- CONSERVATIVE	UNCLASSIFIED	Human Gene SWISSPROT- ACC:P42167 THYMOPOIETINS BETA AND GAMMA (TP BETA AND TP GAMMA) - Homo sapiens (Human), 453 aa.	2.00E-237	12 (12q22)

904	cg43955639	505	CGTGTGGCAGG CATGGTGATGA GGG[G/A]TGCTG GGGCCAGGGAG GTGGCAGGA	G	A	Pro (1277)	Ser (1277)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O15417 CAGL79 - HOMO SAPIENS (HUMAN), 413 aa (fragment).	2.80E-215	
905	cg43950766	991	AGGAATGACCA AAGCACCTGGG TCAT[C]ACTTGT CCACCCACTCTT TAATTTT	T	C	Tyr (1278)	Cys (1278)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD44491 PTD004 - HOMO SAPIENS (HUMAN), 396 aa.	5.30E-214	22
906	cg43985159	2102	ACTTCTGCCTTC AGCTGCAAACC CA[G/A]AGGACG GCATCCGAGGA CTGAACGC	G	A	Ser (1279)	Phe (1279)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q15018 ORF - HOMO SAPIENS (HUMAN), 419 aa (fragment).	1.30E-212	10
907	cg41022625	1136	CGTCTTCTCCAT CATTACATCAT C[G/T]CCACCCT GCTCCTCAGCA CGCAGCT	G	T	Ala (1280)	Ser (1280)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34036 CGI-40 PROTEIN - HOMO SAPIENS (HUMAN), 845 aa.	2.00E-207	11
908	cg44002669	1438	ACCTTGCGCTT GCACCTCGCGGC AGC[C/T]CCTGT CCAGTTCCTCCT TCTCCTTC	C	T	Gly (1281)	Ser (1281)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q16543 CDC37 HOMOLOG - HOMO SAPIENS (HUMAN), 378 aa.	8.80E-205	
909	cg44128902	675	CCGGGATCGAG ACAGAGACAGA GAG[C/G]GGGAC AGGGATCGGGA TCGGGATCG	C	G	Arg (1282)	Gly (1282)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:P18615 RD PROTEIN - Homo sapiens (Human), 380 aa.	1.00E-201	1 (1p36.2)
910	cg44129213	1413	GGGTGTGGACT GGCTGCAGATG TCAT[C]TTGTAA TTCAGATTCTTT CTGGCGA	T	C	Met (1283)	Val (1283)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O88466 ZINC FINGER PROTEIN 106 - MUS MUSCULUS (MOUSE), 1888 aa.	5.60E-194	

911	cg43996402	684	CTTCTCCGGCT CCTTCTCCCT GC[C/A]GTGGCT TCTGCTGCTCC CCTCCTTT	C	A	Gly	Cys (1284)	NON- CONSERVATIVE	UNCLASSIFIED	Human Gene SPTREMBL- ACC:Q12804 RECEPTIN - HOMO SAPIENS (HUMAN), 451 aa.	2.60E-189	2
912	cg43984909	1268	CGAATATCAGCT GCATCCAGTGT CC[C/T]CAGACG AGAATACAAGC CAAGGCCT	C	T	Pro	Leu (1285)	NON- CONSERVATIVE	UNCLASSIFIED	Human Gene SPTREMBL- ACC:Q99963 PROTEIN CONTAINING SH3 DOMAIN, SH3GL3 - HOMO SAPIENS (HUMAN), 347 aa.	1.70E-187	15
913	cg42910688	778	GACAGAGACA TTCCCATATTT TG[G/T]TTGGCA ACAAAAGTGACT TAGTGCG	G	T	Val	Phe (1286)	NON- CONSERVATIVE	UNCLASSIFIED	Human Gene SWISSPROT- ACC:P55040 GTP-BINDING PROTEIN GEM (GTP-BINDING MITOGEN-INDUCED T-CELL PROTEIN) (RAS-LIKE PROTEIN KIR) - Homo sapiens (Human), 296 aa.	7.70E-158	8
914	cg43950590	1351	AAGAATCCTCC GACGGCTTCGT TAC[C/T]ATCCTG TCTGAAGCGGA TTGCACGA	C	T	Gly	Ser (1287)	NON- CONSERVATIVE	UNCLASSIFIED	Human Gene SPTREMBL- ACC:O75323 GBAS - HOMO SAPIENS (HUMAN), 286 aa.	1.90E-154	7
915	cg44931503	945	TTTTAAAGAGTT CATATAATCATA G[A/G]GGTCTTC AAATACCGTTGT TCCTTC	A	G	Leu	Pro (1288)	NON- CONSERVATIVE	UNCLASSIFIED	Human Gene TREMBLNEW- ACC:AAD34078 CGI-83 PROTEIN - HOMO SAPIENS (HUMAN), 288 aa.	5.00E-154	
916	cg43303845	774	ACATTGCCTAGA CAAACTCACAA CT[C/G]ACCTGCT CAAGTTCAAAAT GGCCCA	T	C	Leu	Pro (1289)	NON- CONSERVATIVE	UNCLASSIFIED	Human Gene Homologous to SPTREMBL-ACC:O93263 AVENA - GALLUS GALLUS (CHICKEN), 550 aa.	1.90E-138	
917	cg43973762	117	AGCTGAACAAC AGAAAGTTGTGG AAT[G/T]AGGAG TTAAAATATGCC AGAGGCAA	G	T	Glu	End (1290)	NON- CONSERVATIVE	UNCLASSIFIED	Human Gene Homologous to SPTREMBL-ACC:O14777 RETINOBLASTOMA-ASSOCIATED PROTEIN HEC - HOMO SAPIENS (HUMAN), 642 aa.	2.20E-137	

918	cg43973762	165	CAAGAAGCGA TTGAAACACAAT TA[G/C]CAGAGT ATCACAAATTGG CTAGAAA	G	C	Ala	Pro (1291)	NON- CONSERVATIVE	UNCLASSIFIED	Human Gene Homologous to SPTREMBL-ACC:O14777 RETINOBLASTOMA-ASSOCIATED PROTEIN HEC - HOMO SAPIENS (HUMAN), 642 aa.	2.20E-137
919	cg43973762	376	GCCCTAAATAAA AAATGGGTTTG G[A/G]GGATACT TTAGAACAATTG AATGCA	A	G	Glu	Gly (1292)	NON- CONSERVATIVE	UNCLASSIFIED	Human Gene Homologous to SPTREMBL-ACC:O14777 RETINOBLASTOMA-ASSOCIATED PROTEIN HEC - HOMO SAPIENS (HUMAN), 642 aa.	2.20E-137
920	cg42910848	443	CCATGGTGCCA GGCCGTGCTCC CCA[G/C]GTGCC TCCGGGGTGCT GAAGATCTT	G	C	Pro	Arg (1293)	NON- CONSERVATIVE	UNCLASSIFIED	Human Gene Homologous to SPTREMBL-ACC:O14988 GTPASE- ACTIVATING PROTEIN - HOMO SAPIENS (HUMAN), 308 aa (fragment).	3.10E-132
921	cg29351416	537	TTCCCAAAAGT TCCAAGTAGACA A[C/G]AGTAATC GCCTGTTACTG CAGCAGG	C	G	Asn	Lys (1294)	NON- CONSERVATIVE	UNCLASSIFIED	Human Gene Homologous to SPTREMBL-ACC:Q03626 ALPHA-1- INHIBITOR III PRECURSOR, ISOFORM 2 (RAT PLASMA PROTEINASE INHIBITOR ALPHA-1- INHIBITOR III GROUP 3 VARIANT 36A) (ALPHA-1 PROTEINASE INHIBITOR 3, EXONS 1-4) - RATTUS NORVEGICUS (RAT), 1487 aa.	3.20E-127
922	cg29351416	574	GTTACTGCAGC AGGTCTCAATTAC CA[G/T]ACATTC CTGGGAACATA CCGTCAG	G	T	Asp	Tyr (1295)	NON- CONSERVATIVE	UNCLASSIFIED	Human Gene Homologous to SPTREMBL-ACC:Q03626 ALPHA-1- INHIBITOR III PRECURSOR, ISOFORM 2 (RAT PLASMA PROTEINASE INHIBITOR ALPHA-1- INHIBITOR III GROUP 3 VARIANT 36A) (ALPHA-1 PROTEINASE INHIBITOR 3, EXONS 1-4) - RATTUS NORVEGICUS (RAT), 1487 aa.	3.20E-127
923	cg43938372	481	TTGTTTCCCACT TAATTTATTTTT [C/T]CTGCTTGT CTTCTCTTTCA TCCT	C	T	Gly	Glu (1296)	NON- CONSERVATIVE	UNCLASSIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD40376 PTD013 - HOMO SAPIENS (HUMAN), 243 aa.	1.50E-123

929	cg39512856	344	CTTTTCCAGGC TTCAGCAACG AG[G/A]TTCTTC CTTCGTTGCAAT TTCAG	G	A	Thr (1302)	Ile (1302)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P03740 HYPOTHETICAL PROTEIN ORF194 - Bacteriophage lambda, 194 aa.	1.20E-98	
930	cg39512856	517	GCCGTTCCACTT CTGATATCCCC T[C/T]CCGCCGA TAACCAGGTAAA ATTTC	C	T	Gly (1303)	Glu (1303)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P03740 HYPOTHETICAL PROTEIN ORF194 - Bacteriophage lambda, 194 aa.	1.20E-98	
931	cg39512856	536	TCCCTCCCCG CGATAACCAGG TAA[A/C]ATTTTC CGGTAACGGAC CGAGTTCA	A	C	Phe (1304)	Val (1304)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P03740 HYPOTHETICAL PROTEIN ORF194 - Bacteriophage lambda, 194 aa.	1.20E-98	
932	cg39512856	638	TGGTCTTCAACG AGATGCCACGA TG[C/A]CTCATC ACTGTTGAAAAC AGCCACA	C	A	Ala (1305)	Ser (1305)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P03740 HYPOTHETICAL PROTEIN ORF194 - Bacteriophage lambda, 194 aa.	1.20E-98	
933	cg39570960	851	GCCTCCAGGAA GTCGTTTGTT TG[A/G]GCTGAA CGAATGTGCGT CCAGCCGC	A	G	Glu (1306)	Gly (1306)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O14997 3-7 GENE PRODUCT - HOMO SAPIENS (HUMAN), 709 aa (fragment).	2.60E-93	
934	cg43980391	510	AGTAAATGGACA AGAATATCATCT T[C/T]AACTTGT GACACAGCCGG GCAAGA	C	T	Gln (1307)	End (1307)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q15382 RAS-RELATED GTP- BINDING PROTEIN - HOMO SAPIENS (HUMAN), 184 aa.	2.10E-90	1
935	cg43983527	991	TTCTGGAAGGAT GGTGCACCCTG GT[G/T]CGGCCG CCATTACTGCCA GAGTCTG	G	T	Cys (1308)	Phe (1308)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P47226 TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)] - Mus musculus (Mouse), 423 aa.	6.50E-90	3 (11q23.3)

936	cg42341305	114	GATGAATATTGG AGTACAGACAC AC[C]TGATCC CGCAGCCTAC CTCCAGAA	C	T	Pro	Leu (1309)	NON- CONSERVATIVE	UNCLASSIFIED	Human Gene Similar to SPTREMBL- ACC:O60309 KIAA0563 PROTEIN - HOMO SAPIENS (HUMAN), 870 aa.	8.10E-90
937	cg43980889	737	CTTCTATTTTGA ATTCTAAGACC AT[G]TTACAAGT AGAAAATGATGC TTACC	T	G	His	Gln (1310)	NON- CONSERVATIVE	UNCLASSIFIED	Human Gene Similar to SPTREMBL- ACC:O00581 HYPOTHETICAL 20.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 176 aa.	4.50E-89
938	cg43980889	741	TATTTTGAATTC TAAAGACCAATT A[C]TJAAGTAGA AAATGATGCTTA CCCTGG	C	T	Gln	End (1311)	NON- CONSERVATIVE	UNCLASSIFIED	Human Gene Similar to SPTREMBL- ACC:O00581 HYPOTHETICAL 20.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 176 aa.	4.50E-89
939	cg43980889	781	GCTTACCCTGG TACCGATAGAAC AG[A/C]AAATGTT AAATATAGACAA GTGGAC	A	C	Glu	Ala (1312)	NON- CONSERVATIVE	UNCLASSIFIED	Human Gene Similar to SPTREMBL- ACC:O00581 HYPOTHETICAL 20.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 176 aa.	4.50E-89
940	cg29349483	146	GCAGTTTTTCAC CAAGATCAAGA CC[G/T]CTGACC ACCACTACATG GAGGGCTT	G	T	Ala	Ser (1313)	NON- CONSERVATIVE	UNCLASSIFIED	Human Gene Similar to SPTREMBL- ACC:Q61081 CDC37 HOMOLOG - MUS MUSCULUS (MOUSE), 379 aa.	2.00E-88
941	cg43918287	641	TCTATGGCATCA TCCTGCATGAC CA[C/T]TTGTGC ATCTAAACCAGC CCAGCCG	C	T	Val	Met (1314)	NON- CONSERVATIVE	UNCLASSIFIED	Human Gene Similar to SPTREMBL- ACC:P87891 GAG PROTEIN - HUMAN ENDOGENOUS RETROVIRUS K, 426 aa (fragment).	7.30E-84
942	cg43918287	651	CATCCTGCATGA CCACTTGTGCAT C[T/G]AAACCA CCAGCCGCCA ACCCCCA	T	G	Leu	Phe (1315)	NON- CONSERVATIVE	UNCLASSIFIED	Human Gene Similar to SPTREMBL- ACC:P87891 GAG PROTEIN - HUMAN ENDOGENOUS RETROVIRUS K, 426 aa (fragment).	7.30E-84

943	cg43918287	676	TAAACCAGCCC AGCCGCCAACCC CCC[A/G]AAAGT TGGTCTGCAGTT ATATTAAT	A	G	Leu	Ser (1316)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:P87891 GAG PROTEIN - HUMAN ENDOGENOUS RETROVIRUS K, 426 aa (fragment).	7.30E-84	
944	cg43918287	693	CAACCCCAAA AGTTGGTCTGC AGTT/CJATATTA ATTGAGGTTGG ACCTGGG	T	C	Ile	Met (1317)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:P87891 GAG PROTEIN - HUMAN ENDOGENOUS RETROVIRUS K, 426 aa (fragment).	7.30E-84	
945	cg37027086	217	GAATCAGAACTA CAAGGATCAATT A/T/CJCCAGCT CAATGTCAGGG TTCCTCA	T	C	Ser	Pro (1318)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:BAA76824 KIAA0980 PROTEIN - HOMO SAPIENS (HUMAN), 1406 aa (fragment).	1.20E-83	
946	cg42688841	430	ATTATAACTGGG ATCCAGTCAAC A/T/AJAGGTAG AATTTCAATTAAC CTCAAG	T	A	Met	Leu (1319)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:Q02380 NADH-UBIQUINONE OXIDOREDUCTASE SGD SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-SGDH) (CI-SGDH) - Bos taurus (Bovine), 189 aa.	1.90E-83	
947	cg42688841	598	CCGAGCCTAGT GCCAGCGCGGC GGC[A/C]AGACA GAGCTGTCAGA GCGGCGACC	A	C	Cys	Gly (1320)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:Q02380 NADH-UBIQUINONE OXIDOREDUCTASE SGD SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-SGDH) (CI-SGDH) - Bos taurus (Bovine), 189 aa.	1.90E-83	
948	cg40332814	339	ACTGCACAGGG ACCGAATCTCTG CC/T/CJCCCGCT CTGCAGCCAGG TGCTCCAA	T	C	Glu	Gly (1321)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:BAA74864 KIAA0841 PROTEIN - HOMO SAPIENS (HUMAN), 641 aa (fragment).	3.10E-83	19
949	cg43920571	2059	GCGTTTTTCTCT CACGTCCGTCT GA[G/A]ATTACT GAGGAATATTGT GCTGGC	G	A	Ser	Phe (1322)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P34624 HYPOTHETICAL 63.5 KD PROTEIN ZK353.1 IN CHROMOSOME III - Caenorhabditis elegans, 548 aa.	3.50E-82	10

950	cg44024149	451	GGAAGCCGCAC TCAGTTATGGCT TC[T/C]ACGGCT GCCACTGTGGC GTGGGTGG	T	C	Tyr	His (1323)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P14555 PHOSPHOLIPASE A2, MEMBRANE ASSOCIATED PRECURSOR (EC 3.1.1.4) (PHOSPHATIDYLCHOLINE 2- ACYLHYDROLASE) (GROUP II PHOSPHOLIPASE A2) - Homo sapiens (Human), 144 aa.	5.30E-79	1 (1p35)
951	cg43307245	156	GATATGATAGCT TGTCCTGAAACT G[A/G]GACTCCT GCCGTGATAAC GTGTGAC	A	G	Glu	Gly (1324)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O15488 GLYCOGENIN-2 ALPHA - HOMO SAPIENS (HUMAN), 501 aa.	1.00E-75	X
952	cg39523553	698	GTGTGAGGTTCT GCCCAGATCCGG GAT[G/A]GCTGC CGGTGGGTGAT CGACGGTAG	G	A	Gly	Ser (1325)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:CAB40855 PUTATIVE ADENINE GLYCOSYLASE - STREPTOMYCES COELICOLOR, 308 aa.	7.20E-75	
953	cg39523553	861	ATGGCTCTTTCC GCCTGGCCCCGA GCT[T/C]CGATCA GGCATCAAGGT GCCTGGAA	T	C	Leu	Pro (1326)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:CAB40855 PUTATIVE ADENINE GLYCOSYLASE - STREPTOMYCES COELICOLOR, 308 aa.	7.20E-75	
954	cg35933325	312	ACCAAATGCCA CTATTTTTCTC CC[A/C]TTGCCA AAAATGAAGGAA ATCACGT	A	C	Asn	Lys (1327)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:BAA74845 KIAA0822 PROTEIN - HOMO SAPIENS (HUMAN), 1581 aa.	2.40E-74	
955	cg41677120	325	CACGACCCACG AGATCATGGGG CCC[A/G]AGAAA AAGCACCTGGA CTACTTAAT	A	G	Lys	Glu (1328)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q13492 CALM (TYPE I CALM PROTEIN) - HOMO SAPIENS (HUMAN), 652 aa.	1.10E-71	11

956	cg41677120	330	CCCACGAGATC ATGGGGCCCAA GAA/A/C/JAAGCA CCTGGACTACTT AATTCAGT	A	C	Lys	Asn (1329)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q13492 CALM (TYPE I CALM PROTEIN) - HOMO SAPIENS (HUMAN), 652 aa.	1.10E-71	11
957	cg41677120	382	CACAAATGAGAT GAATGTGAACAT C/C/TJACACAGTT GGCAGACAGTT TATTGA	C	T	Pro	Ser (1330)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q13492 CALM (TYPE I CALM PROTEIN) - HOMO SAPIENS (HUMAN), 652 aa.	1.10E-71	11
958	cg39648832	208	TGCAGCCTCGT CCTCCTCCTCTG GC[A/T]GGCTCT GCACACTCTGC TCCTGGTA	A	T	Leu	Gln (1331)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:BAA76807 KIAA0963 PROTEIN - HOMO SAPIENS (HUMAN), 1366 aa.	3.20E-70	
959	cg42696021	412	GACACCCGCAC CCGGGCATGCT TCA[C/G]ACAGT GGCTGTGCCGC CTTCACAAAT	C	G	Thr	Arg (1332)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P55789 AUGMENTER OF LIVER REGENERATION (HERV1 PROTEIN) - Homo sapiens (Human), 125 aa.	1.40E-69	
960	cg42696021	421	ACCCGGGCATG CTTCACACAGTG GC[T/C]GTGCCG CCTTCACAATGA AGTGAAC	T	C	Leu	Pro (1333)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P55789 AUGMENTER OF LIVER REGENERATION (HERV1 PROTEIN) - Homo sapiens (Human), 125 aa.	1.40E-69	
961	cg34243633	269	CAGAGATAATG CAGGCCAGGGA GGA[G/C]ATTGC ACTGGATGTCA CCATCATGG	G	C	Ile	Met (1334)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O88552 CLAUDIN-2 - MUS MUSCULUS (MOUSE), 230 aa.	1.30E-68	

968	cg44938009	1289	GAGTGCACGCA TAAAGATGGAA GAG[G/T]ATGCA CTACTTTCTGAT CCAGTGGA	G	T	Asp	Tyr (1341)	NON- CONSERVATIVE	UNCLASSIFIED	Human Gene Similar to SWISSNEW- ACC:O43182 RHO-GTPASE- ACTIVATING PROTEIN 6 (RHO- TYPE GTPASE-ACTIVATING PROTEIN RHOGAPX-1) - Homo sapiens (Human), 587 aa.	5.80E-66	X
969	cg43949821	287	ATTTTAATTCCT TCCTGTCTACG GC[G/A]GTTGGA CCTCCTGGCTC TCIGCIGT	G	A	Arg	Cys (1342)	NON- CONSERVATIVE	UNCLASSIFIED	Human Gene Similar to TREMBLNEW-ACC:AAD34394 NUCLEAR PORE COMPLEX INTERACTING PROTEIN NPIP - HOMO SAPIENS (HUMAN), 350 aa.	3.80E-62	
970	cg39516123	681	TGGCTTCGGCT GGCGGGCCATC AAT[C/T]CCAGC ATGGCTGCCCC CAGCAGTCC	C	T	Pro	Ser (1343)	NON- CONSERVATIVE	UNCLASSIFIED	Human Gene Similar to SWISSPROT- ACC:Q04205 TENSIN - Gallus gallus (Chicken), 1744 aa.	5.10E-62	
971	cg42731307	347	CGAAAAGCAAA GTGCAGTTTGTT GC[T/C]TCGGCT GTTGAGTGGTT CGGGTCCA	T	C	Ser	Gly (1344)	NON- CONSERVATIVE	UNCLASSIFIED	Human Gene Similar to SWISSPROT- ACC:Q99653 CALCIUM-BINDING PROTEIN P22 (CALCIUM-BINDING PROTEIN CHP) - Homo sapiens (Human), 194 aa.	2.60E-61	
972	cg42731307	488	TCTGGAAGAA GGCATTGATGAT CC[G/A]GTCCCC CAGTGGGTTGA TGGCAAGT	G	A	Arg	Trp (1345)	NON- CONSERVATIVE	UNCLASSIFIED	Human Gene Similar to SWISSPROT- ACC:Q99653 CALCIUM-BINDING PROTEIN P22 (CALCIUM-BINDING PROTEIN CHP) - Homo sapiens (Human), 194 aa.	2.60E-61	
973	cg42731307	524	GGGTTGATGGC AAGTTCTGGAAT CC[T/C]CTGGAA ATCTCCCGGCT GAGAGTC	T	C	Arg	Gly (1346)	NON- CONSERVATIVE	UNCLASSIFIED	Human Gene Similar to SWISSPROT- ACC:Q99653 CALCIUM-BINDING PROTEIN P22 (CALCIUM-BINDING PROTEIN CHP) - Homo sapiens (Human), 194 aa.	2.60E-61	
974	cg44910937	648	TGCCTTTGGAAC AGGAATATGAAA A[G/T]AAACTCA GAGCCGAGTTA GTGAAA	G	T	Lys	Asn (1347)	NON- CONSERVATIVE	UNCLASSIFIED	Human Gene Similar to SPTREMBL- ACC:Q20716 F53B7.3 - CAENORHABDITIS ELEGANS, 267 aa.	2.60E-61	3

975	cg43335624	149	TCGAAAGGAAG TGAGTGCAGAT GGG[A/G]AGACC ATCACTGTCAC TTCCTTAA	A	G	Lys	Glu (1348)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q62184 T-COMPLEX PROTEIN 10C (TCP-10) - MUS MUSCULUS (MOUSE), 438 aa.	7.00E-61	
976	cg43277268	448	CGCTAATGCCA AGAAGGAGATG GTG[C/A]GCTCC AAGCTGCCCAA CAGTGTGCT	C	A	Arg	Ser (1349)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:AAD45423 EH DOMAIN-CONTAINING PROTEIN EHD1 - MUS MUSCULUS (MOUSE), 534 aa.	3.90E-60	
977	cg44128084	724	CTTGACATCCAG CCAGACGGTTC AG[A/G]ATCAGC GGTCTGTGGT GCGACGGG	A	G	Glu	Gly (1350)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O33196 HYPOTHETICAL 32.9 KD PROTEIN - MYCOBACTERIUM TUBERCULOSIS, 307 aa.	1.70E-59	
978	cg30455661	322	TTCTCAAGTGGT TTGAAGTCAAAC AIG[T/A]TTCAAC AGAAGAAATCA GCCCTC	G	T	Gln	His (1351)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q14185 DOCK180 PROTEIN - HOMO SAPIENS (HUMAN), 1865 aa.	5.20E-58	
979	cg42747615	31	TGTGATAAAAGT CACTTTCAGGC CA[T/C]TCACAG CGAATCTTCAGA CACITTT	T	C	Ile	Thr (1352)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q14693 HYPOTHETICAL PROTEIN KIAA0188 - Homo sapiens (Human), 899 aa (fragment).	1.60E-57	
980	cg43153425	276	ACAAATTACTAT GGGTTCTACTG AA[T/G]CTCGGG TTGACTACATGG GCTCAAG	T	G	Ser	Ala (1353)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:BAA83061 KIAA1109 PROTEIN - HOMO SAPIENS (HUMAN), 1957 aa (fragment).	2.40E-57	
981	cg43968980	1093	TATTTCTGCTT CTCTAACAGCTG A[C/A]TGTAATT GCTTCCTTGA CTGAAG	C	A	Ser	Ile (1354)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60925 PREFOLDIN SUBUNIT 1 - HOMO SAPIENS (HUMAN), 122 aa.	2.50E-56	

982	cg30384142	173	GATAGTGGTGT GTGGTGATGCG AGT[A/T]AACCT GACGAATGGTT AGCTGAAAT	A	T	Lys	End (1355)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P44788 SUN PROTEIN (FMU PROTEIN) - Haemophilus influenzae, 451 aa.	5.30E-56	
983	cg43957773	445	GGGCTCACCGT AGAGCAACTGC AAT[C/A]GCTCT GGGCTGGGCC TGGACAGGA	C	A	Asp	Tyr (1356)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O43914 DNAX ACTIVATION PROTEIN 12 - HOMO SAPIENS (HUMAN), 113 aa.	3.30E-54	19
984	cg43931038	464	AGGGCAACTTG TGGGCAACCTG GTC[A/C]AGGAA ACCTTGACTTCT TCAAAATTC	A	C	Leu	Trp (1357)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O46082 EG:63B12.2 PROTEIN - DROSOPHILA MELANOGASTER (FRUIT FLY), 254 aa.	6.10E-54	11
985	cg43931038	588	CCTCCCCCAT GCGATGCCCAA CAC[T/C]TTTGC GAGTGATGGC TTGAAAGGG	T	C	Ser	Gly (1358)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O46082 EG:63B12.2 PROTEIN - DROSOPHILA MELANOGASTER (FRUIT FLY), 254 aa.	6.10E-54	11
986	cg43971060	686	CCCACCTCGTT CGTGCTCCAC CCT[C/T]CCCAG CTCCACCGCCT GGTCTTCAG	C	T	Pro	Ser (1359)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P31639 SODIUM/GLUCOSE COTRANSPORTER 2 (NA(+)/GLUCOSE COTRANSPORTER 2) (LOW AFFINITY SODIUM-GLUCOSE COTRANSPORTER) - Homo sapiens (Human), 672 aa.	4.20E-53	
987	cg44010070	541	TTCTCTGCCGG CACCTACCCGC GCC[T/G]GGAGG AGTACCGCCGG GGCATCTTA	T	G	Leu	Arg (1360)	NON- CONSERVATI VE	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:O35775 SYNCOLLIN (SIP9) - Rattus norvegicus (Rat), 145 aa.	6.40E-51	

988	cg43298242	145	TCTGTTGGCAG GGCTCACAGAG ACG[G/A]GGGTG AGGGGAGAGAT CGTGGGTTC	G	A	Pro	Leu (1361)	NON- CONSERVATIVE	water_channel	Human Gene SWISSPROT- ID:O14520 AQUAPORIN-7 LIKE (AQUAPORIN ADIPOSE) (AQPA) - HOMO SAPIENS (HUMAN), 342 aa.	1.30E-163	
989	cg43298242	163	AGAGACGGGG TGAGGGGAGAG ATC[G/A]TGGT TCATGAGATCCC ATCTTGGG	G	A	Thr	Met (1362)	NON- CONSERVATIVE	water_channel	Human Gene SWISSPROT- ID:O14520 AQUAPORIN-7 LIKE (AQUAPORIN ADIPOSE) (AQPA) - HOMO SAPIENS (HUMAN), 342 aa.	1.30E-163	
990	cg43300636	440	CCACAGCCGCC ACGCCACCTC CCG[G/gap]CCC AGGCCAGGCC TATGCCCATCA	G	gap	Gly	Gly (1363)	FRAMESHIFT	ATPase-associated	Human Gene SPTREMBL-ID:Q29466 VACUOLAR H+-ATPASE SUBUNIT (EC 3.6.1.34) (H(+)-TRANSPORTING ATP SYNTHASE) (H(+)- TRANSPORTING ATPASE) (MITOCHONDRIAL ATPASE) (CHLOROPLAST ATPASE) (COUPLING FACTORS (F(O), F(1) AND CF(1))) - BOS TAURUS (BOVINE), 838 aa.	1.70E-175	
991	cg43300636	446	CCGCCACGCC ACCTCCCGGCC CAG[G/gap]CCCCA GGCCTATGCGC ATCACCATGG	G	gap	Gly	Gly (1364)	FRAMESHIFT	ATPase-associated	Human Gene SPTREMBL-ID:Q29466 VACUOLAR H+-ATPASE SUBUNIT (EC 3.6.1.34) (H(+)-TRANSPORTING ATP SYNTHASE) (H(+)- TRANSPORTING ATPASE) (MITOCHONDRIAL ATPASE) (CHLOROPLAST ATPASE) (COUPLING FACTORS (F(O), F(1) AND CF(1))) - BOS TAURUS (BOVINE), 838 aa.	1.70E-175	
992	cg43250373	193	CTGTGGGGTTG ACCCAGAACAA AGC[A/gap]TTGC CAGAAACGTTA AGTATGGGA	A	gap	Leu	Cys (1365)	FRAMESHIFT	ATPase-associated	Human Gene Similar to TREMBLNEW-ID:G2921585 ECTO- ATPASE - MUS MUSCULUS (MOUSE), 495 aa.	1.40E-100	10 (10q24)

993	cg43132502	360	GGCCCCAGTGC AGTGGGTGGCA CCG[C/gap]CGA GGCTGCTGTTA CGGCTCATCTT	C	gap	Pro	Arg (1366)	FRAMESHIFT	ATPase_ associat ed	Human Gene Similar to SPTREMBL- ID:Q15332 GAMMA SUBUNIT OF SODIUM POTASSIUM ATPASE LIKE - HOMO SAPIENS (HUMAN), 126 aa.	9.40E-58	11
994	cg42528468	284	GCTCCTGCCTG GGAACAACCGG AAG[G/gap]TGTA TGAAGTGAAGCA ATGTGCAAGA	G	gap	Val	Cys (1367)	FRAMESHIFT	cadherin	Human Gene Similar to SWISSPROT- ID:P05362 INTERCELLULAR ADHESION MOLECULE-1 PRECURSOR (ICAM-1) (MAJOR GROUP RHINOVIRUS RECEPTOR) (CD54) - HOMO SAPIENS (HUMAN), 532 aa.	8.40E-78	19 (19p13.3)
995	cg43264626	1150	TTTGCCAGTTTT CTTCTTGAGTTG G[C/gap]CCTCCA GGGCACCCACA GAGCTAAA	C	gap	Gly	Ala (1368)	FRAMESHIFT	cathepsi n	Human Gene SWISSPROT- ID:P43235 CATHEPSIN K PRECURSOR (EC 3.4.22.38) (CATHEPSIN O) (CATHEPSIN X) (CATHEPSIN O2) - HOMO SAPIENS (HUMAN), 329 aa.	4.10E-183	1
996	cg43132668	1893	CGATGCGTGCC AGGGTGATTCC GGA[G/gap]GCC CGCTGGTGTGT GAGGACCAAGC	G	gap	Gly	Ala (1369)	FRAMESHIFT	cathepsi n	Human Gene Similar to SWISSPROT- ID:P98119 SALIVARY PLASMINOGEN ACTIVATOR ALPHA 1 PRECURSOR (EC 3.4.21.68) (DSPA ALPHA-1) - DESMODUS ROTUNDUS (VAMPIRE BAT), 477 aa.	3.90E-74	5 (5q33)
997	cg43132668	1894	GATGCGTGCCA GGGTGATTCCG GAG[G/gap]CCC GCTGGTGTGTG AGGACCAAGCT	G	gap	Gly	Ala (1370)	FRAMESHIFT	cathepsi n	Human Gene Similar to SWISSPROT- ID:P98119 SALIVARY PLASMINOGEN ACTIVATOR ALPHA 1 PRECURSOR (EC 3.4.21.68) (DSPA ALPHA-1) - DESMODUS ROTUNDUS (VAMPIRE BAT), 477 aa.	3.90E-74	5 (5q33)
998	cg44924334	198	AAAGCTAATTGA GACCTATTCTC C[A/gap]AAAACT ACCAAGACTATG AGTATCT	A	gap	Lys	Lys (1371)	FRAMESHIFT	glycoprot ein	Human Gene Similar to SWISSPROT- ID:Q13491 NEURONAL MEMBRANE GLYCOPROTEIN M6-B - HOMO SAPIENS (HUMAN), 283 aa (fragment).	5.60E-76	

999	cg43303165	2549	GGCCCCCACTA TCAGGGGCCCT GGC[C/gap]TCAA TCACTGAGACC ATCCAAGTCC	C	gap	Ser	Gln (1372)	FRAMESHIFT	histone	Human Gene Similar to SWISSPROT- ID:P53973 HISTONE DEACETYLASE HDA1 - SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST), 706 aa.	4.10E-70	X
1000	cg42489148	881	TGCGAGTGGAT GCGGAACCGGC GCA[G/gap]CAGT CCCTCGGCAGC CAAGTGAAAA	G	gap	Ser	Thr (1373)	FRAMESHIFT	homeobox	Human Gene Homologous to SPTREMBL-ID:O00503 CAUDAL- TYPE HOMEBOX PROTEIN 2 - HOMO SAPIENS (HUMAN), 313 aa.	6.00E-118	13
1001	cg43929210	483	TCTGGCTCAGC ATGATGTTCCCT CT[G/gap]GCCTT CAGCCTGCCAC TAAAGAATG	G	gap	Ala	Ala (1374)	FRAMESHIFT	hydroxysteroid	Human Gene SWISSPROT- ID:P51659 ESTRADIOL 17 BETA- DEHYDROGENASE 4 (EC 1.1.1.62) (17-BETA-HSD 4) (17-BETA- HYDROXYSTEROID DEHYDROGENASE 4) - HOMO SAPIENS (HUMAN), 736 aa.	0.00E+00	5
1002	cg44004587	1811	GCTTATTTTCGG TGTTGAATAAGA A[G/gap]ACACTA AAAGCTCGATG CAATAATC	G	gap	Val	Val (1375)	FRAMESHIFT	isomerase	Human Gene Homologous to SPTREMBL-ID:Q13907 HOMOLOG OF YEAST IPP ISOMERASE - HOMO SAPIENS (HUMAN), 228 aa.	3.00E-123	
1003	cg41501665	156	CGCTTCTCCAA GGTGCTGGAGG AGG[C/gap]GGC GGCCGCCGAGG AGGGCCTGCC	C	gap	Ala	Gly (1376)	FRAMESHIFT	kinase	Human Gene Similar to TREMBLNEW-ID:D1025880 ZIP- KINASE - HOMO SAPIENS (HUMAN), 454 aa.	2.70E-76	
1004	cg41501665	184	CGGCCGCCGAG GAGGGCCTGCG CGA[G/gap]CTGC AGCGCAGCCGG CGGCTCTGCC	G	gap	Leu	Cys (1377)	FRAMESHIFT	kinase	Human Gene Similar to TREMBLNEW-ID:D1025880 ZIP- KINASE - HOMO SAPIENS (HUMAN), 454 aa.	2.70E-76	

1011	cg42488873	494	GTCAGCATAGT GCCCATTTTG GGG[C/gap]ATCC TTCAGCTGGAC AAGGGAACA	C	gap	Cys	Ser (1384)	FRAMESHIFT	lipase	Human Gene SWISSPROT- ID:P54317 PANCREATIC LIPASE RELATED PROTEIN 2 PRECURSOR (EC 3.1.1.3) - HOMO SAPIENS (HUMAN), 469 aa.	9.80E-261	
1012	cg42488873	923	CACGGGGCCCC CCAGCCTCCTG CCC[G/gap]CCTC CGCGGCCGTGT GCGGCCCCAG	G	gap	Ala	Gly (1385)	FRAMESHIFT	lipase	Human Gene SWISSPROT- ID:P54317 PANCREATIC LIPASE RELATED PROTEIN 2 PRECURSOR (EC 3.1.1.3) - HOMO SAPIENS (HUMAN), 469 aa.	9.80E-261	
1013	cg43249083	2329	GGAGCAGCTCC AGGAGACGCTG CTG[C/gap]GGG CTCTTCGGGCT CTGGTGCTGAA	C	gap	Arg	Gly (1386)	FRAMESHIFT	nuc_l_rec pt	Human Gene SWISSPROT- ID:P20393 V-ERBA RELATED PROTEIN EAR-1 - HOMO SAPIENS (HUMAN), 614 aa.	0.00E+00	17 (17q11.2)
1014	cg43991048	6644	TCCTTCCTTTCTT CTCTCTTTTCTT C/gap]TGTTTTT CTGCTTTATCCT CTTCT	C	gap	Glu	Lys (1387)	FRAMESHIFT	nuc_l_rec pt	Human Gene SPTREMBL-ID:Q60974 NUCLEAR RECEPTOR CO- REPRESSOR - MUS MUSCULUS (MOUSE), 2453 aa.	0.00E+00	17
1015	cg43919677	4055	GAAGAAAAGAA AGAATGCTACTA TA[A/gap]TCTCA ATGACGCCAGT CTCTGTGAT	A	gap	Asn	Ile (1388)	FRAMESHIFT	oncogen e	Human Gene SWISSPROT- ID:Q00918 LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1 PRECURSOR (TRANSFORMING GROWTH FACTOR BETA-1 BINDING PROTEIN 1) (TGF-BETA1- BP- 1) (TRANSFORMING GROWTH FACTOR BETA-1 MASKING PROTEIN, LARGE SUBUNIT) - RATTUS NORVEGICUS (RAT), 1712 aa.	0	2 (2p12)

1034	cg43927750	2857	TAAAAGTTATTC TCCAATGGTGAT T[G/gap]GGCAAG CCCTGCCTCCT GTATTCCT	G	gap	Pro (1407)	Pro	FRAMESHIFT	UNCLAS SIFIED	Human Gene SWISSNEW- ACC:Q13496 MYOTUBULARIN - Homo sapiens (Human), 603 aa.	0	X (Xq28)
1035	cg43961075	1344	GGTAGGATTG CTCATTTCAGGG CA[G/gap]CTGTC GCAAGCATCTC CCACCCCGT	G	gap	Ser (1408)	Ser	FRAMESHIFT	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:P49746 THROMBOSPONDIN 3 PRECURSOR - Homo sapiens (Human), 956 aa.	0	1
1036	cg43961763	1192	CATCTAGGTCAA CAGGAAGGTCA AG[C/gap]TCCCG CTCCGGTTCCA CTGATCCAT	C	gap	Asp (1409)	Glu	FRAMESHIFT	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:P13521 SECRETOGRANIN II PRECURSOR (SGII) (CHROMOGRANIN C) - Homo sapiens (Human), 617 aa.	0	2
1037	cg43968223	2979	GTTCTGTTCTTG TAGCGCTTTCTG C[G/gap]CTGCAG CATGATCTGAAG CTTGTTG	G	gap	Ala (1410)	Arg	FRAMESHIFT	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O60342 KIAA0602 PROTEIN - HOMO SAPIENS (HUMAN), 962 aa (fragment).	0	14
1038	cg43980727	2673	CCCTCCAGGTA GAGGCCTAGGA AGG[C/gap]CCCA GAACTGAAGCC GAAGCGCTGG	C	gap	Pro (1411)	Ala	FRAMESHIFT	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:P38432 P80-COILIN - Homo sapiens (Human), 576 aa.	0	17
1039	cg43999667	3941	TTCTGTTTGTG AGGACTTTTTT T[T/gap]CTACAA GTTGTTTTCTG GGATCAC	T	gap	Glu (1412)	Glu	FRAMESHIFT	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O60281 KIAA0530 PROTEIN - HOMO SAPIENS (HUMAN), 1563 aa (fragment).	0	6
1040	cg44022781	3927	GTATCAAGTGC TCCTTCCAACTT T[T/gap]GGAGGC CCCATCACCAC ACCGGTA	T	gap	Pro (1413)	Pro	FRAMESHIFT	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q14692 KIAA0187 PROTEIN - HOMO SAPIENS (HUMAN), 1282 aa.	0	

1041	cg44919370	571	CGTGGACTTTTC	C	gap	Leu	Trp (1414)	FRAMESHIFT	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O60624 CLASS I CYTOKINE RECEPTOR - HOMO SAPIENS (HUMAN), 636 aa.	0	19
1042	cg44932924	2612	TCTACAACCCAGA GCCAGGAATTA CA[G/gap]IACGAA GCTGGAGGACT GCAGGAACA	G	gap	Thr	Arg (1415)	FRAMESHIFT	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q92574 HAMARTIN (MYELOBLAST KIAA0243) - HOMO SAPIENS (HUMAN), 1164 aa.	0	9
1043	cg43991434	1167	GGGGTGCAAGG GCCTTGGGGAA ATA[G/gap]TCCT GCTGCACCATG TGGTTCAGCG	G	gap	Asp	Asp (1416)	FRAMESHIFT	UNCLAS SIFIED	Human Gene SWISSNEW- ACC:P46060 RAN-GTPASE ACTIVATING PROTEIN 1 - Homo sapiens (Human), 587 aa.	1.7E-304	22
1044	cg44931278	1264	CCTCCTCCAGG GAAGCACTGGC CAG[G/gap]TCCT GCAGTGTAGGC CACTTCTGCA	G	gap	Asp	Asp (1417)	FRAMESHIFT	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:Q15830 MUTY HOMOLOG - HOMO SAPIENS (HUMAN), 535 aa.	4.5E-280	1
1045	cg43949042	427	CACAGCTGCGT TGCCATAGTTGC CC[T/gap]GGAAA AAGCGGCCCCAC GAACCCAGGC	T	gap	Gln	Arg (1418)	FRAMESHIFT	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O75907 ACAT RELATED GENE PRODUCT 1 - HOMO SAPIENS (HUMAN), 488 aa.	6.10E-268	
1046	cg43972066	2313	TAAATTGACTT TTCATCATGTAA A[A/gap]TGCTA ATGCGATGTATT TGGTAAT	A	gap	His	His (1419)	FRAMESHIFT	UNCLAS SIFIED	Human Gene SPTREMBL- ACC:O60747 PUTATIVE G-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 562 aa (fragment).	4.10E-221	10

1053	cg44004690	402	ACCGGAGAGTG GGCACCCCGTC CCA[G/gap]GGG CCATTCTTCGA GGGAGCACCA	G	gap	Gly (1426)	FRAMESHIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA74892 KIAA0869 PROTEIN - HOMO SAPIENS (HUMAN), 888 aa (fragment).	2.50E-161	
1054	cg43957283	322	TCGAGGGTGAC CACAGCCCCAG AGG[G/gap]CCG CAGCACAGCGC AGGGGGTGGCG	G	gap	Pro (1427)	FRAMESHIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD27734 CGI-25 PROTEIN - HOMO SAPIENS (HUMAN), 301 aa.	1.40E-160	
1055	cg43329741	336	GCTCTACCTGG GCTACACCCCG CAG[G/gap]CGG CCCGTGAAGTG CGCATCATGCA	G	gap	Arg (1428)	FRAMESHIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD39906 FH1/FH2 DOMAIN- CONTAINING PROTEIN FHOS - HOMO SAPIENS (HUMAN), 1164 aa.	6.70E-159	
1056	cg44010310	501	TTTGTTGAGATG CATGAATTTTT T[gap]/TCTCTATT GCTGCTTGAAA TTTACA	gap	T	Lys (1429)	FRAMESHIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA32101 BCAP - HOMO SAPIENS (HUMAN), 331 aa.	1.30E-155	13
1057	cg39729127	981	GCTCTCTCTTT ATTGGTAACCG T[gap]/TGGTGGC CACGAGTCATA CAGGGAAA	gap	T	Val (1430)	FRAMESHIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD42876 NY-REN-45 ANTIGEN - HOMO SAPIENS (HUMAN), 815 aa.	3.00E-152	1
1058	cg43135797	861	AGATCTGCTCC CCGGAGACCCG GA[G/gap]CCGCT GGCCATTGCAG AAGGCGCCC	G	gap	Ser (1431)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:O14732 MYO- INOSITOL-1(OR 4)- MONOPHOSPHATASE 2 (EC 3.1.3.25) (IMP 2) (INOSITOL MONOPHOSPHATASE 2) (MYO- INOSITOL MONOPHOSPHATASE A2) - Homo sapiens (Human), 288 aa.	1.60E-150	18

1071	cg42530218	329	ATTAATACACA GCAGCAGCAGC AA[A/gap]CTACA TTAGGTGGTCTC TTCAGTCA	A	gap	Thr	Leu (1444)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P70582 NUCLEOPORIN P54 - RATTUS NORVEGICUS (RAT), 510 aa.	2.00E-118	
1072	cg43325007	979	AGGATACCCCC GAGGAAGGCCG CCA[G/gap]GAAT GCGTGTGCTGG GTAGGTCTTG	G	gap	Leu	Trp (1445)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD43195 PEROXISOMAL MEMBRANE PROTEIN PMP 24 - HOMO SAPIENS (HUMAN), 212 aa.	4.80E-110	20
1073	cg43981269	776	GGCCTACGGCG CCTACGCTCAG GCA[C/gap]TGAT GCAGCAGCAAG CGGCCCTGAT	C	gap	Leu	End (1446)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q91579 RIBONUCLEOPROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 462 aa.	4.50E-105	
1074	cg43250166	166	AGGTGGCCCTC ACACCCAGTGC TGT[G/gap]CTGC GCGGAGGGCTG TACTGAAGGT	G	gap	Ala	Asp (1447)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB43382 HYPOTHETICAL 146.2 KD PROTEIN - HOMO SAPIENS (HUMAN), 1296 aa.	3.30E-102	2
1075	cg43982164	778	CTGCGGCGGGT GCTCATCCTGG ACA[gap/C]ATTC ACCTGCCTCCTA TGCTTTCCA	gap	C	Asn	Thr (1448)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O15194 HYA22 - HOMO SAPIENS (HUMAN), 340 aa.	1.00E-90	
1076	cg43980889	812	TTAAATATAGAC AAGTGGACCAT TT[gap]GCCTCA AATTCACAGGA GCCAGCAT	T	gap	Ala	Pro (1449)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O00581 HYPOTHETICAL 20.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 176 aa.	4.50E-89	

1077	cg43970119	832	GTGGCCATTGG TGAGACATCCAT CA[A/gap]TATTG CAAACCAAAAGT TTTATTTTC	A	gap	Ile	Met (1450)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O88719 CMP-N- ACETYLNEURAMINIC ACID SYNTHETASE (EC 2.7.7.43) (ACYLNEURAMINATE CYTIDYLTRANSFERASE) (CMP- SIALATE PYROPHOSPHORYLASE) (CMP-SIALATE SYNTHASE) - MUS MUSCULUS (MOUSE), 432 aa.	1.00E-82	12
1078	cg44030987	447	TCGGCATGTTG AGTGGAAACAGT TGTTA[gap]TTTA CTTGAATCCAA TCTCCTTCT	A	gap	Tyr	Thr (1451)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:BAA76495 TYPE II MEMBRANE PROTEIN SIMILAR TO CD69 - HOMO SAPIENS (HUMAN), 149 aa.	1.90E-81	
1079	cg43320682	665	GGTGCTCAGG GGCTGGGGGAG GCT[C/gap]CCCT GGGGCTTCAGA CAGCACATAG	C	gap	Glu	Ser (1452)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:CAB45773 HYPOTHETICAL 18.0 KD PROTEIN - HOMO SAPIENS (HUMAN), 162 aa (fragment).	6.60E-81	
1080	cg25255686	366	AAGGCACCATC AAGTCGGCGGT GGC[C/gap]TTCG GGCATCTCCTT GCCGAGGGTA	C	gap	Phe	Ser (1453)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:CAB39700 CONSERVED HYPOTHETICAL PROTEIN - STREPTOMYCES COELICOLOR, 384 aa.	2.10E-77	
1081	cg43988975	371	CTCCTCCTGAC CGAGTGGGCGG GCA[G/gap]GAG CTTGAATCGTC ATTGGAGATG	G	gap	Glu	Ser (1454)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P50606 MAGO NASHI PROTEIN HOMOLOG - Homo sapiens (Human), and Mus musculus (Mouse), 146 aa.	8.00E-76	
1082	cg39523553	670	CACTGGTATGC ACGGCGCGGTC TCC[G/gap]CAGT GTGAGGTCCTGC CCGATCCGGG	G	gap	Gln	Ser (1455)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:CAB40855 PUTATIVE ADENINE GLYCOSYLASE - STREPTOMYCES COELICOLOR, 308 aa.	7.20E-75	

1083	cg43951096	2953	CTCCCTCCTGG GTATCTGCATCT TC[gap]/AJAAAAT CTCCTTCTTGGT TTTCATCC	gap	A	Glu	End (1456)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q23382 ZK1058.4 - CAENORHABDITIS ELEGANS, 442 aa.	2.00E-71	17
1084	cg42831353	806	GGACACAGGCT GCGGTGTAAGC CCG[C/gap]GTCA CCGCCGGCACC TGCAGGAACT	C	gap	Thr	Thr (1457)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:AAD37863 PUTATIVE NADH OXIDOREDUCTASE COMPLEX I SUBUNIT - CAENORHABDITIS ELEGANS, 237 aa.	1.30E-67	22
1085	cg44938009	688	AATACTCCGTGC AGCGAGTGCGT CA[G/gap]CTCCG TGAAGAAITTTGA TCAAGGTC	G	gap	Leu	Ser (1458)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:O43182 RHO-GTPASE- ACTIVATING PROTEIN 6 (RHO- TYPE GTPASE-ACTIVATING PROTEIN RHOGAPX-1) - Homo sapiens (Human), 587 aa.	5.80E-66	X
1086	cg43054992	315	CAAAATCACAGC TGAAGAAATGTA T[G/gap]ATATAT TTGGGAAATATG GACCTAT	G	gap	Asp	Ile (1459)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:AAD34105 CGI- 110 PROTEIN - HOMO SAPIENS (HUMAN), 125 aa.	4.60E-64	2
1087	cg39516123	928	CCTGGGGCTCA CCAAGGCAACC TGG[C/gap]CTCC GGTCTTCATAGC AATGCAATA	C	gap	Ala	Ala (1460)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q04205 TENSIN - Gallus gallus (Chicken), 1744 aa.	5.10E-62	
1088	cg43983590	713	GGAGGAGCCAG GCGAGCACACC CCC[C/gap]TGT GGCCCCCTGCCA CGGCCCCAGCC	C	gap	Leu	Cys (1461)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q19498 SIMILAR TO MELIBIOSE CARRIER PROTEIN - CAENORHABDITIS ELEGANS, 501 aa.	1.50E-60	

1089	cg44128084	499	CGGCGGCGCAT GCTCGACGTTT TGG[C/gap]GTCT GTCGACGAGTT GCCGGTGCAA	C	gap	Ala	Gly (1462)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O33196 HYPOTHETICAL 32.9 KD PROTEIN - MYCOBACTERIUM TUBERCULOSIS, 307 aa.	1.70E-59	
1090	cg44128084	524	CGTCTGTCGAC GAGTTGCCGGT GCA[A/gap]CGCT GGAGCTGCGAC GGGATCCTGG	A	gap	Arg	Ala (1463)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O33196 HYPOTHETICAL 32.9 KD PROTEIN - MYCOBACTERIUM TUBERCULOSIS, 307 aa.	1.70E-59	
1091	cg43976473	931	GGCCCTGTGCT TGGAGCCCGTGG GCT[C/gap]CGTA GCCCGAGTGAT AAGCCATGCG	C	gap	Gly	Glu (1464)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O35946 HYPOTHETICAL 14.9 KD PROTEIN - RATTUS NORVEGICUS (RAT), 137 aa.	3.50E-59	11
1092	cg40309770	385	TTCCGGCCGCC GCGTCCAGGGC TCG[C/gap]CCGC TGAGGTCGTTT ATGACCCCGC	C	gap	Gly	Gly (1465)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q60870 POLYPOSIS LOCUS PROTEIN 1 HOMOLOG (TB2 PROTEIN HOMOLOG) (GP106) - Mus musculus (Mouse), 185 aa.	4.10E-56	
1093	cg42725664	184	AGATAGCTGAG AATATTCTGCGC AA[G/gap]CCTCA CAGCTTGTTC TGGCAGCC	G	gap	Leu	Leu (1466)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:BAA74896 KIAA0873 PROTEIN - HOMO SAPIENS (HUMAN), 466 aa (fragment).	1.5E-51	
1094	cg39380052	497	ATGAGATCGAC GCCTTGCGCGG CCG[C/gap]GGC GTAGACATTCC GCACCCGCTCA	C	gap	Gly	Ala (1467)	FRAMESHIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW-ACC:CAB42016 PUTATIVE ADENYLOSUCCINATE SYNTHETASE - STREPTOMYCES COELICOLOR, 427 aa.	1.3E-50	

1095	cg44928804	1181	CTCTCAATCATG CCGCTTTAGAG AA[T/gap]GCAAC ATGGGCAACCT GATTTGTGA	T	gap	Cys	Ala (1468)	FRAMESHIFT	UNCLAS SIFIED	Human Gene SWISSPROT- ACC:P21589 5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) (ECTO- NUCLEOTIDASE) (5'-NT) (CD73 ANTIGEN) - Homo sapiens (Human), 574 aa.	9.1e-313	6 (6q14)
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